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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:25:40 ; Search time 94.5296 Seconds
(without alignments)
878.681 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 215
Sequence: 1 IAVEYDDTQFLRFSDDAAI.....QRGSEQTQTELVTETRPAG 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	215	11	US-09-819-371-6
2	119	55.3	271	9	US-09-925-301-1431
3	119	55.3	274	11	US-09-819-371-5
4	119	55.3	362	15	US-10-257-021-82
5	119	55.3	442	16	US-10-408-765A-1887
6	95	44.2	362	11	US-09-819-371-4
7	55	25.6	96	14	US-10-029-386-30718
8	52	24.2	186	15	US-10-264-049-4063
9	32	14.9	91	9	US-09-864-761-35461
10	32	14.9	110	9	US-09-796-692-799
11	32	14.9	110	9	US-09-796-692-2139
					Sequence 6, Appli
					Sequence 1431, Ap
					Sequence 5, Appli
					Sequence 82, Appli
					Sequence 1887, Ap
					Sequence 4, Appli
					Sequence 30718, A
					Sequence 4063, Ap
					Sequence 35461, A
					Sequence 799, App
					Sequence 2139, Ap

12	14.9	110	14	US-10-040-862-799	Sequence 799, App
13	14.9	110	14	US-10-040-862-2139	Sequence 2139, Ap
14	14.9	110	15	US-10-057-475B-799	Sequence 799, App
15	14.9	110	15	US-10-057-475B-2139	Sequence 2139, Ap
16	14.9	110	15	US-10-154-884B-799	Sequence 799, App
17	14.9	110	15	US-10-154-884B-2139	Sequence 2139, Ap
18	14.9	110	16	US-10-764-324-799	Sequence 799, App
19	14.9	110	16	US-10-764-324-2139	Sequence 2139, Ap
20	14.9	110	16	US-10-262-839-48	Sequence 48, Appl
21	14.9	198	15	US-10-264-049-3505	Sequence 3505, Ap
22	14.9	365	17	US-10-741-600-941	Sequence 941, App
23	14.0	104	9	US-09-925-302-835	Sequence 835, App
24	14.0	104	10	US-09-925-302-835	Sequence 835, App
25	14.0	371	15	US-10-085-198-72	Sequence 72, Appl
26	14.0	371	15	US-10-210-172-156	Sequence 156, App
27	13.0	91	14	US-10-029-386-31089	Sequence 31089, A
28	13.0	476	16	US-10-430-984-16	Sequence 16, Appl
29	13.0	500	16	US-10-430-984-15	Sequence 15, Appl
30	10.7	77	14	US-10-029-386-34273	Sequence 34273, A
31	10.7	96	14	US-10-029-386-28377	Sequence 28377, A
32	8.8	136	16	US-10-425-115-363890	Sequence 363890,
33	7.9	184	9	US-09-858-580-21	Sequence 21, Appl
34	7.9	184	10	US-09-847-172-21	Sequence 21, Appl
35	7.9	184	17	US-10-941-152-21	Sequence 21, Appl
36	7.9	421	15	US-10-138-588-32	Sequence 32, Appl
37	7.9	421	15	US-10-210-172-174	Sequence 174, App
38	7.4	91	9	US-09-864-761-38005	Sequence 38005, A
39	7.4	92	15	US-10-380-880-5	Sequence 5, Appli
40	7.4	145	9	US-09-810-560-8	Sequence 8, Appli
41	7.4	198	16	US-10-741-601-387	Sequence 387, App
42	7.4	198	17	US-10-741-601-1143	Sequence 1143, Ap
43	7.4	234	15	US-10-380-880-8	Sequence 8, Appli
44	7.4	251	16	US-10-741-601-384	Sequence 384, App
45	7.4	251	17	US-10-741-600-1142	Sequence 1142, Ap

ALIGNMENTS

RESULT 1

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca
; FILE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 100.0%; Score 215; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.4e-203;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IAVEYDDTQFLRFSDDAAI PRMEPREPWVEGQPOYWEWTTGYAKANAQTDRVALRNLL 60
Db 1 IAVEYDDTQFLRFSDDAAI PRMEPREPWVEGQPOYWEWTTGYAKANAQTDRVALRNLL 60
QY 61 RRYNQEAGSHTLQGNMGCDMGDGLRLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 120
Db 61 RRYNQEAGSHTLQGNMGCDMGDGLRLRGYHQHAWDKDYISLNEDLSRWTAAADTVAQI 120
QY 121 TORFYEAEYAEFFRTYLEGECLELLRRYLENGKETLQRPADPPKAHVAHPISDHEATLR 180
Db 121 TORFYEAEYAEFFRTYLEGECLELLRRYLENGKETLQRPADPPKAHVAHPISDHEATLR 180

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QY 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 181 CWALGFYPAEITLTWQDGEQTDTELVTETPAG 215

RESULT 2
US-09-925-301-1431
; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431

Query Match 55.3%; Score 119; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 156
Db 146 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 205

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 206 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 264

RESULT 3
US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match 55.3%; Score 119; DB 11; Length 274;
Best Local Similarity 100.0%; Pred. No. 2e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 156
Db 119 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 178

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 179 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 237
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RESULT 4
US-10-257-021-82
; Sequence 82, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

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Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 199

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
Db 200 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 258

RESULT 5
US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101674A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1887

Query Match 55.3%; Score 119; DB 16; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 156
Db 140 DGKDYISLNEDLSRSTAADTVAQITQRFYEAEYAEFFRTYLEGECLELLRRYLENGKET 199

QY 157 LQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEQTDTELVTETPAG 215
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Db 200 LQADPPKAVHHPISDHEATLRCWALGFYPAIBITLTWQRDGEQTDTELVTETPAG 258

RESULT 6

US-09-819-371-4

; Sequence 4, Application US/09819371

; Publication No. US20040053344A1

; GENERAL INFORMATION:

; APPLICANT: Egawa, Kohji

; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can

; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819,371

; CURRENT FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-819-371-4

Query Match

Best Local Similarity 44.2%; Score 95; DB 11; Length 362;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44 IAVEYVDVDTQFLRDSDAALPRMPREPWEQEGFPQYWEWTTGYAKANAQTDRLVALRNLL 103

Qy 61 RRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHA 95

Db 104 RRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQHA 138

RESULT 7

US-10-029-386-30718

; Sequence 30718, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

; SEQ ID NO 30718

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR6.1

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12

; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52

US-10-029-386-30718

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Best Local Similarity 25.6%; Score 55; DB 14; Length 96;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 DPPKAVHHPISDHEATLRCWALGFYPAIBITLTWQRDGEQTDTELVTETPAG 215

Db 2 DPPKAVHHPISDHEATLRCWALGFYPAIBITLTWQRDGEQTDTELVTETPAG 56

RESULT 8

US-10-264-049-4063

; Sequence 4063, Application US/10264049

Query Match

Best Local Similarity 24.2%; Score 52; DB 15; Length 186;

US-10-264-049-4063

; Publication No. US20040005579A1

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA133P1

; CURRENT APPLICATION NUMBER: US/10/264,049

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/18569

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: US 60/209,467

; PRIOR FILING DATE: 2000-06-07

; NUMBER OF SEQ ID NOS: 4360

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 4063

; LENGTH: 186

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (76)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (77)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (86)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (107)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (123)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (124)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (136)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (148)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (163)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (174)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (175)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

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; NAME/KEY: MISC FEATURE

; LOCATION: (176)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (180)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

;/ PRIOR FILING DATE: 2000-08-07
;/ PRIOR APPLICATION NUMBER: US 09/796,692
;/ PRIOR FILING DATE: 2001-03-01
;/ NUMBER OF SEQ ID NOS: 10467
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 2139
;/ LENGTH: 110
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-10-040-862-2139

Query Match 14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 14
US-10-057-475B-799

;/ Sequence 799, Application US/10057475B
;/ Publication No. US20040002068A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Gaiger, Alexander
;/ APPLICANT: Algate, Paul A.
;/ APPLICANT: Mannion, Jane
;/ APPLICANT: Clapper, Jonathan David
;/ APPLICANT: Wang, Aijun
;/ APPLICANT: Ordenez, Nadia
;/ APPLICANT: Carter, Lauren
;/ APPLICANT: McNeill, Patricia Dianne
;/ APPLICANT: Corixa Corporation
;/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;/ FILE REFERENCE: 014058-014402US
;/ CURRENT APPLICATION NUMBER: US/10/057,475B
;/ CURRENT FILING DATE: 2002-01-22
;/ PRIOR APPLICATION NUMBER: US 60/186,126
;/ PRIOR FILING DATE: 2000-03-01
;/ PRIOR APPLICATION NUMBER: US 60/190,479
;/ PRIOR FILING DATE: 2000-03-17
;/ PRIOR APPLICATION NUMBER: US 60/200,545
;/ PRIOR FILING DATE: 2000-04-27
;/ PRIOR APPLICATION NUMBER: US 60/200,303
;/ PRIOR FILING DATE: 2000-04-28
;/ PRIOR APPLICATION NUMBER: US 60/200,779
;/ PRIOR FILING DATE: 2000-04-28
;/ PRIOR APPLICATION NUMBER: US 60/200,999
;/ PRIOR FILING DATE: 2000-05-01
;/ PRIOR APPLICATION NUMBER: US 60/206,201
;/ PRIOR FILING DATE: 2000-05-22
;/ PRIOR APPLICATION NUMBER: US 60/218,950
;/ PRIOR FILING DATE: 2000-07-14
;/ PRIOR APPLICATION NUMBER: US 60/222,903
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 10979
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 799
;/ LENGTH: 110
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-10-057-475B-799

Query Match 14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200

Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 15
US-10-057-475B-2139

;/ Sequence 2139, Application US/10057475B
;/ Publication No. US20040002068A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Gaiger, Alexander
;/ APPLICANT: Algate, Paul A.
;/ APPLICANT: Mannion, Jane
;/ APPLICANT: Clapper, Jonathan David
;/ APPLICANT: Wang, Aijun
;/ APPLICANT: Ordenez, Nadia
;/ APPLICANT: Carter, Lauren
;/ APPLICANT: McNeill, Patricia Dianne
;/ APPLICANT: Corixa Corporation
;/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
;/ FILE REFERENCE: 014058-014402US
;/ CURRENT APPLICATION NUMBER: US/10/057,475B
;/ CURRENT FILING DATE: 2002-01-22
;/ PRIOR APPLICATION NUMBER: US 60/186,126
;/ PRIOR FILING DATE: 2000-03-01
;/ PRIOR APPLICATION NUMBER: US 60/190,479
;/ PRIOR FILING DATE: 2000-03-17
;/ PRIOR APPLICATION NUMBER: US 60/200,545
;/ PRIOR FILING DATE: 2000-04-27
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;/ PRIOR FILING DATE: 2000-04-28
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;/ PRIOR APPLICATION NUMBER: US 60/202,084
;/ PRIOR FILING DATE: 2000-05-04
;/ PRIOR APPLICATION NUMBER: US 60/206,201
;/ PRIOR FILING DATE: 2000-05-22
;/ PRIOR APPLICATION NUMBER: US 60/218,950
;/ PRIOR FILING DATE: 2000-07-14
;/ PRIOR APPLICATION NUMBER: US 60/222,903
;/ PRIOR FILING DATE: 2000-08-03
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 10979
;/ SOFTWARE: FastSeq for Windows Version 3.0
;/ SEQ ID NO 2139
;/ LENGTH: 110
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-10-057-475B-2139

Query Match 14.9%; Score 32; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

Search completed: July 13, 2005, 09:46:00
Job time : 94.5296 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:15:29 ; Search time 17.1472 Seconds
(without alignments)
935.984 Million cell updates/sec

Title: US-09-819-371-6
Perfect score: 215
Sequence: 1 IAVEYDDTQFLRFDSDAAI.....QRDGEQTQDTLVELTRPAG 215

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfilei.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	55.3	362	4	US-09-949-016-8242
2	77	35.8	120	4	US-09-513-999C-4290
3	32	14.9	274	1	US-08-222-851-1
4	28	13.0	358	4	US-09-949-016-6620
5	28	13.0	360	4	US-09-949-016-8370
6	17	7.9	184	3	US-09-153-586-21
7	17	7.9	184	4	US-09-558-580-21
8	16	7.4	117	2	US-08-406-057-9
9	16	7.4	117	3	US-08-958-316-9
10	16	7.4	145	2	US-08-406-057-8
11	16	7.4	145	3	US-08-958-316-8
12	16	7.4	338	4	US-09-949-016-6176
13	16	7.4	339	4	US-09-949-016-8636
14	16	7.4	361	3	US-08-652-265-22
15	16	7.4	361	3	US-08-834-497A-22
16	16	7.4	361	3	US-09-503-444A-22
17	15	7.0	92	4	US-09-673-809-25
18	15	7.0	182	1	US-08-127-954-135
19	15	7.0	182	1	US-08-127-954-151
20	15	7.0	274	2	US-08-484-905-105
21	15	7.0	274	2	US-08-484-905-106
22	15	7.0	274	2	US-08-484-905-107
23	15	7.0	274	2	US-08-484-905-108
24	15	7.0	274	3	US-08-481-985B-105
25	15	7.0	274	3	US-08-481-985B-106
26	15	7.0	274	3	US-08-481-985B-107
27	15	7.0	274	3	US-08-481-985B-108

28	15	7.0	274	3	US-08-370-476-105	Sequence 105, App
29	15	7.0	274	3	US-08-370-476-106	Sequence 106, App
30	15	7.0	274	3	US-08-370-476-107	Sequence 107, App
31	15	7.0	274	3	US-08-370-476-108	Sequence 108, App
32	15	7.0	341	3	US-08-890-719-38	Sequence 38, Appl
33	15	7.0	365	2	US-08-484-905-97	Sequence 97, Appl
34	15	7.0	365	2	US-08-484-905-98	Sequence 98, Appl
35	15	7.0	365	2	US-08-484-905-99	Sequence 99, Appl
36	15	7.0	365	2	US-08-484-905-100	Sequence 100, App
37	15	7.0	365	2	US-08-484-905-101	Sequence 101, App
38	15	7.0	365	2	US-08-484-905-102	Sequence 102, App
39	15	7.0	365	2	US-08-484-905-103	Sequence 103, App
40	15	7.0	365	2	US-08-484-905-104	Sequence 104, App
41	15	7.0	365	3	US-08-481-985B-97	Sequence 97, Appl
42	15	7.0	365	3	US-08-481-985B-98	Sequence 98, Appl
43	15	7.0	365	3	US-08-481-985B-99	Sequence 99, Appl
44	15	7.0	365	3	US-08-481-985B-100	Sequence 100, App
45	15	7.0	365	3	US-08-481-985B-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-09-949-016-8242
; Sequence 8242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CL001307
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8242
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8242

Query Match 55.3%; Score 119; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.5e-111;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 DGVYISLNEIDRSWTAADTVAQITQRFYEABEYAEFFTYLGECELELRRYLENGKET 156
DB 140 DGVYISLNEIDRSWTAADTVAQITQRFYEABEYAEFFTYLGECELELRRYLENGKET 199
QY 157 LQRADEPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 215
DB 200 LQRADEPKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 258

RESULT 2
US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLILLSGALUT/DT
US-09-513-999C-4290

Query Match 35.8%; Score 77; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-69; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;
QY 1 IAVEYDDTQFLRFSDAAIPRMEPREPWVEGQYWEWTTGYAKANAQTDRLVALRNL 60
Db 44 IAVEYDDTQFLRFSDAAIPRMEPREPWVEGQYWEWTTGYAKANAQTDRLVALRNL 103
QY 61 RRYNOSEAGSHTLQGN 77
Db 104 RRYNOSEAGSHTLQGN 120

RESULT 3
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRNFOERSWSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-1

Query Match 14.9%; Score 32; DB 1; Length 274;

Best Local Similarity 100.0%; Pred. No. 6.2e-24; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 0;
QY 169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
Db 191 HHPISDHEATLRCWALGFYPAEITLTWQDGE 222
RESULT 4
US-09-949-016-6620
; Sequence 6620, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6620
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6620

Query Match 13.0%; Score 28; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 7.8e-20; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;
QY 169 HHPISDHEATLRCWALGFYPAEITLTWQ 196
Db 212 HHPISDHEATLRCWALGFYPAEITLTWQ 239

RESULT 5
US-09-949-016-8370
; Sequence 8370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8370
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8370

Query Match 13.0%; Score 28; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.9e-20; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;
QY 169 HHPISDHEATLRCWALGFYPAEITLTWQ 196

Db 214 HHPISDHEATLRCWALGFYPABEITLWQ 241

RESULT 6
US-09-153-586-21
; Sequence 21, Application US/09153586A
; Patent No. 6270772
; GENERAL INFORMATION:
; APPLICANT: Burrows et al.
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of
; TITLE OF INVENTION: antigen-specific T-Cells
; FILE REFERENCE: 48823
; CURRENT APPLICATION NUMBER: US/09/153,586A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: 60/064,552
; EARLIER FILING DATE: 1997-09-16
; EARLIER APPLICATION NUMBER: 60/064,555
; EARLIER FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-153-586-21

Query Match 7.9%; Score 17; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LRRYLENGKETLQADP 162
|||
Db 168 LRRYLENGKETLQADP 184
|||

RESULT 7
US-09-858-580-21
; Sequence 21, Application US/09858580
; Patent No. 6815171
; GENERAL INFORMATION:
; APPLICANT: Burrows et al.
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of
; TITLE OF INVENTION: antigen-specific T-Cells
; FILE REFERENCE: 48823
; CURRENT APPLICATION NUMBER: US/09/858,580
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/153,586
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/064,552
; PRIOR FILING DATE: 1997-09-16
; PRIOR APPLICATION NUMBER: 60/064,555
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-580-21

Query Match 7.9%; Score 17; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 LRRYLENGKETLQADP 162
|||
Db 168 LRRYLENGKETLQADP 184
|||

RESULT 8
US-08-406-057-9
; Sequence 9, Application US/08406057
; Patent No. 5856442

; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,057
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-331-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-057-9

Query Match 7.4%; Score 16; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPABI 191
|||
Db 20 EATLRCWALGFYPABI 35
|||

RESULT 9
US-08-958-316-9
; Sequence 9, Application US/08958316
; Patent No. 6291659
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: Tape
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/958,316
/ FILING DATE: 27-OCT-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 94 03179
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 0846-0437-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 117 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-958-316-9

Query Match 7.4%; Score 16; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
Db 20 EATLRCWALGFYPAEI 35

RESULT 10
US-08-406-057-8
/ Sequence 8, Application US/08406057
/ Patent No. 5856442
/ GENERAL INFORMATION:
/ APPLICANT: CAROSELLA, EDGARDO D
/ APPLICANT: MOREAU, PHILIPPE
/ APPLICANT: GLUCKMAN, ELIANE
/ APPLICANT: KIRSZENBAUM, MAREK
/ TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
/ TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
/ NUMBER OF SEQUENCES: 15
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
/ STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: USA
/ ZIP: 2202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Tape
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/406,057
/ FILING DATE: 17-MAR-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 94 03179
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 846-331-0
/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 145 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-406-057-8

Query Match 7.4%; Score 16; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
Db 48 EATLRCWALGFYPAEI 63

RESULT 11
US-08-958-316-8
/ Sequence 8, Application US/08958316
/ Patent No. 6291659
/ GENERAL INFORMATION:
/ APPLICANT: CAROSELLA, EDGARDO D
/ APPLICANT: MOREAU, PHILIPPE
/ APPLICANT: GLUCKMAN, ELIANE
/ APPLICANT: KIRSZENBAUM, MAREK
/ TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
/ TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
/ STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
/ CITY: ARLINGTON
/ STATE: VIRGINIA
/ COUNTRY: USA
/ ZIP: 2202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Tape
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/958,316
/ FILING DATE: 27-OCT-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 94 03179
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 0846-0437-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 145 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-958-316-8

Query Match 7.4%; Score 16; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
|||||
Db 48 EATLRCWALGFYPAEI 63

RESULT 12
US-09-949-016-6176
; Sequence 6176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6176
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6176

Query Match 7.4%; Score 16; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
|||||
Db 222 EATLRCWALGFYPAEI 237

RESULT 13
US-09-949-016-8636
; Sequence 8636, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8636
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8636

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Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
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Db 223 EATLRCWALGFYPAEI 238

RESULT 14
US-08-652-265-22
; Sequence 22, Application US/08652285
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..361
; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
US-08-652-265-22

Query Match 7.4%; Score 16; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 222 EATLRCWALGFYPAEI 237

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; Sequence 22, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Pennie & Edmonds LLP
3 STREET: 1155 Avenue of the Americas
4 CITY: New York
5 STATE: New York
6 COUNTRY: USA
7 ZIP: 10036-2811
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC Compatible
11 OPERATING SYSTEM: Windows 95
12 SOFTWARE: FastSEQ for Windows Version 2.0b
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/834,497A
15 FILING DATE: 04-APR-1997
16 CLASSIFICATION: 514
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/652,265
19 FILING DATE: 23-MAY-1996
20 CLASSIFICATION: 514
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/632,673
23 FILING DATE: 16-APR-1996
24 CLASSIFICATION: 514
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/630,912
27 FILING DATE: 04-APR-1996
28 CLASSIFICATION: 514
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Poissant, Brian M.
31 REGISTRATION NUMBER: 28,462
32 REFERENCE/DOCKET NUMBER: 8907-0056-999
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 650-493-4935
35 TELEFAX: 650-493-5556
36 TELEX: 66141 PENNIE
37 INFORMATION FOR SEQ ID NO: 22:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 361 amino acids
40 TYPE: amino acid
41 STRANDEDNESS:
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44 FEATURE:
45 NAME/KEY: Protein
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47 OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
48 US-08-834-497A-22

Query Match 7.4%; Score 16; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 EATLRCWALGFYPAEI 191
Db 222 EATLRCWALGFYPAEI 237

Search completed: July 13, 2005, 09:29:10
Job time : 18.1472 secs

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OM protein - protein search, using sw model.

Run on: July 13, 2005, 08:59:16 ; Search time 169 Seconds
(without alignments)
1096.880 Million cell updates/sec

Title: US-09-819-371-4
Perfect score: 362
Sequence: 1 MAPRSLLLLSGALALTDTW.....QAAVTDSAGQSGVSLTANKV 362

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	261	72.1	362	1	HLAF_HUMAN
2	245	67.7	346	2	Q8WLP5
3	244	67.4	460	2	Q95HC0
4	232	64.1	346	2	Q6DU28
5	223	61.6	324	2	Q861E9
6	223	61.6	324	2	Q861F0
7	196	54.1	254	2	Q860R0
8	174	48.1	346	2	Q8MGQ1
9	148	40.9	349	2	Q6DU20
10	148	40.9	349	2	Q6DUW0
11	113	31.2	346	1	1C28_PANTR
12	113	31.2	346	2	Q95V72
13	113	31.2	362	2	Q7YR27
14	87	24.0	91	2	Q9TPX7
15	73	20.2	316	2	Q29958
16	62	17.1	314	2	Q860F6
17	61	16.9	353	2	Q9MXS6
18	61	16.9	353	2	Q9MXS7
19	61	16.9	354	2	Q70UE5
20	61	16.9	354	2	Q70UE6
21	61	16.9	354	2	Q70UE7
22	61	16.9	365	2	Q66ST5
23	61	16.9	365	2	Q9MXS5
24	59	16.3	59	2	Q78094
25	59	16.3	348	1	HLAF_MACMU
26	58	16.0	354	2	Q70S10
27	58	16.0	365	2	Q617A3
28	55	15.2	365	2	Q617A9
29	53	14.6	354	2	Q70SH4
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31	50	13.8	351	2	Q70P17

32	50	13.8	351	2	Q70PM0
33	46	12.7	355	2	Q767W6
34	45	12.4	330	2	Q30713
35	45	12.4	338	2	Q95510
36	45	12.4	359	2	Q30711
37	44	12.2	91	2	Q7YNY3
38	44	12.2	91	2	Q7YNY6
39	44	12.2	91	2	Q7YF25
40	44	12.2	91	2	Q9MYH8
41	44	12.2	91	2	Q9MYI0
42	44	12.2	91	2	Q9MYI2
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ALIGNMENTS

RESULT 1
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ID HLAF_HUMAN STANDARD; PRT; 362 AA.
AC P30511; Q9TP68;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDA12).
GN Name=HLA-F; Synonyms=HLA-5.4, HLAF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90111605; PubMed=1688605;
RA Geraghty D.E., Wei X., Orr H.T., Koller B.H.;
RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element."
RL J. Exp. Med. 171:1-18(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91197889; PubMed=1707659;
RA Lury D., Epstein H., Holmes N.;
RT "The human class I MHC gene HLA-F is expressed in lymphocytes."
RL Int. Immunol. 2:531-537(1990).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20189617; PubMed=10727083;
RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcelet M., Mottier S., Dreano S., Gatiou M.T., Hitt C., Soriano N., Galibert F.;
RT "A 356-Kb sequence of the subtelomeric part of the MHC class I region."
RL DNA Seq. 10:263-299(1999).
[4]
RP SEQUENCE FROM N.A.
RX Shima S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A., AND VARIANT PRO-272.
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E., Gilbert J.G.R., Clamp M.B., Bethel G., Milne S., Ainscough R., Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S., Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P., Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.V., Burford D.C., Burrill W., Burton J., Carder C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V., Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

FT	VARIANT	272	272	S -> P (in dbSNP-1736924) .
FT				/FTID=VAR_018327.
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Best Local Similarity 99.7%; Pred. No. 3 3e-243;				
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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Db	1	MAPRSLLLSSGALALTD	TWAGSHSLRYFSTAVSR	PGRGEPRIYAVEYVDDTQFLRFDS 60
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Db	61	AAIPRMEPRPWEQGPQW	ETTYGAKANAQTDRLVAL	NLLRRNQSEAGSHTLQGMN 120
Qy	121	GCDMGPDGRLRLGYHQA	YDVKDYISNEDLRSWTA	ADTVAQITQRFYEAEVEEPRTY 180
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Qy	181	LEGECELELLRRYLENG	LETIQRADPPKHAHHP	IPSDHEATLRCWALGFYPAEITLTWQR 240
Db	181	LEGECELELLRRYLENG	LETIQRADPPKHAHHP	IPSDHEATLRCWALGFYPAEITLTWQR 240
Qy	241	DGEQEQDTLVELVTRPA	GDTFOKWAAVVPSGEE	QRYTCHVQHEGLPQPLILRWESQP 300
Db	241	DGEQEQDTLVELVTRPA	GDTFOKWAAVVPSGEE	QRYTCHVQHEGLPQPLILRWESQP 300
Qy	301	PTPIVIGIVAGLVVLGA	VNTGAVVAAMVRKSS	DRNRGYSOAAVTDSAQGGVSLTAN 360
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Qy	361	KV 362		
Db	361	KV 362		
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AC	Q8WLP5			
DT	01-MAR-2002 (T-EMBLrel. 20, Created)			
DT	01-MAR-2002 (T-EMBLrel. 20, Last sequence update)			
DT	25-OCT-2004 (T-EMBLrel. 28, Last annotation update)			
DE	MHC class Ib antigen (HLA-F protein).			
GN	Name=HLA-F;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RA	SEQUENCE FROM N.A.			
RA	He X., Xu L., Liu Y., Zeng Y.;			
RX	PubMed=14705989;			
RT	Identification of a novel HLA-F allele - HLA-F*010102.;			
RL	Tissue Antigens 63:181-183 (2004).			
RN	[3]			
RA	SEQUENCE FROM N.A.			
RA	He X., Xu L., Liu Y., Zeng Y.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
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RA	SEQUENCE FROM N.A.			
RA	TISSUE=Lymph;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Reingold E.A., Grouse L.H., Detge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,			

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
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 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
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 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF523285; AM74980.1; -
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 DR GO; GO:0006955; P:immune response; IEA.
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 DR PRINTS; PR01638; MHC_I.1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; ICG1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Transmembrane.
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 Best Local Similarity 99.7%; Pred. No. 9.2e-228;
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QY 61 AAI PRPEPWPVEQSPQWETTTGAKANAQTDRLVALNLLRRYNSAGSHTLQGMN 120
 DB 61 AAI PRPEPWPVEQSPQWETTTGAKANAQTDRLVALNLLRRYNSAGSHTLQGMN 120
 QY 121 GCDMGPDGRLRGYHGHVGDGKDYISLNEDLRSWTAADTVAQITQRYEAEVEAEFRY 180
 DB 121 GCDMGPDGRLRGYHGHVGDGKDYISLNEDLRSWTAADTVAQITQRYEAEVEAEFRY 180
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 DB 181 LEGECLELRRYLENGLETLQADPPKAVHHPISDHEATLRCWALGFPYPAETTLTQW 240
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 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE HLA-F protein (Fragment).
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dlatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
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 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009260; AAH09260.2; -
 DR HSP; Q3TQH5; 1B0R.
 DR GO; GO:0016020; C:membrane; IEA.
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 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00129; MHC_I; 1.

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FT NON_TER 1
SQ SEQUENCE 460 AA; 52263 MW; 1A0B6891978D93E CRC64;

Query Match
Best Local Similarity 67.4%; Score 244; DB 2; Length 460;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPRSLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDS 60
Db 19 MAPRSLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDS 78
QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNSQSEAGSHTLQGN 120
Db 79 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNSQSEAGSHTLQGN 138
QY 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFRTY 180
Db 139 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFRTY 198
QY 181 LECELELLRRYLENGLETQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240
Db 199 LECELELLRRYLENGLETQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 258
QY 241 DSEEQTDTELVTETPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQ 300
Db 259 DSEEQTDTELVTETPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQ 318
QY 301 PTPIVIGVAGVVLGAVVTGAVAAVMWRKSSDRNRGSYQAA 345
Db 319 PTPIVIGVAGVVLGAVVTGAVAAVMWRKSSDRNRGSYQAA 363

RESULT 4
Q6DU28 PRELIMINARY; PRT; 346 AA.
AC Q6DU28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pyo C.-W., Ishitani A., Moore Y.F., Garaghty D.E.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY645747; AAT73230.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;

Query Match
Best Local Similarity 64.1%; Score 232; DB 2; Length 346;

Best Local Similarity 99.7%; Pred. No. 1.1e-226;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 LALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAI PRMEPREPV 73
Db 14 LALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAI PRMEPREPV 73
QY 74 BOEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNSQSEAGSHTLQGNMGCDMGPDGRLRG 133
Db 74 BOEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNSQSEAGSHTLQGNMGCDMGPDGRLRG 133
QY 134 YHQHAYDGKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFRTYLECELELLRRYL 193
Db 134 YHQHAYDGKDYISLNEDLSWTAADTVAQITQRFYEAEYAEFFRTYLECELELLRRYL 193
QY 194 ENGETLQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRGEEQTQDTLVE 253
Db 194 ENGETLQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRGEEQTQDTLVE 253
QY 254 TRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQPTPIVIGVAGLV 313
Db 254 TRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQPTPIVIGVAGLV 313
QY 314 VLGA VVTGAVAAVMWRKSSDRNRGSYQAAV 346
Db 314 VLGA VVTGAVAAVMWRKSSDRNRGSYQAAV 346

RESULT 5
Q6BL1E9 PRELIMINARY; PRT; 324 AA.
AC Q6BL1E9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY221102; AAC34407.1; -
DR HSP; Q9TQH5; 1B0R.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001039; MHC I.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR PRINTS; PRO1638; MHCCLASSI.
DR ProDom; PD000050; MHC I; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
SQ NON_TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match
Best Local Similarity 61.6%; Score 223; DB 2; Length 324;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SILLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSAAIP 64
Db 1 SILLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSAAIP 60
QY 65 RMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNSQSEAGSHTLQGNMGCDM 124

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Db      61  RMEPRFWVEQEGQYWEWTTGYAKANAQTDVLRVLRNLLRRYNSAGSHTLQMGCDM 120
Qy      125  GPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTYLEGE 184
Db      121  GPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTYLEGE 180
Qy      185  CLELLRRYLENGLETQADPPKKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 244
Db      181  CLELLRRYLENGLETQADPPKKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 240
Qy      245  QTQDTLTVETRPAGDGTFFQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRWESQPQTIP 304
Db      241  QTQDTLTVETRPAGDGTFFQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRWESQPQTIP 300
Qy      305  IVGIVAGLVVLGAVVTGAVVAAM 328
Db      301  IVGIVAGLVVLGAVVTGAVVAAM 324

RESULT 6
Q861FO ID Q861FO PRELIMINARY; PRT; 324 AA.
AC Q861FO;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DE Nonclassical MHC class I antigen (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216882; AAC37689.1; -.
DR HSSP; Q9TQHS; 1B0R.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 61.6%; Score 223; DB 2; Length 324;
Best Local Similarity 99.7%; Pred. No. 1.6e-206;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  SLILLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAIP 64
Db      1  SLILLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSDAIP 60
Qy      65  RMEPRFWVEQEGQYWEWTTGYAKANAQTDVLRVLRNLLRRYNSAGSHTLQMGCDM 124
Db      61  RMEPRFWVEQEGQYWEWTTGYAKANAQTDVLRVLRNLLRRYNSAGSHTLQMGCDM 120
Qy      125  GPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTYLEGE 184
Db      121  GPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTYLEGE 180
Qy      185  CLELLRRYLENGLETQADPPKKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 244

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Db      181  CLELLRRYLENGLETQADPPKKAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 240
Qy      245  QTQDTLTVETRPAGDGTFFQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRWESQPQTIP 304
Db      241  QTQDTLTVETRPAGDGTFFQKAAVAVVPSGEEQRYTCHVQHEGLPQPLILRWESQPQTIP 300
Qy      305  IVGIVAGLVVLGAVVTGAVVAAM 328
Db      301  IVGIVAGLVVLGAVVTGAVVAAM 324

RESULT 7
Q860RO ID Q860RO PRELIMINARY; PRT; 254 AA.
AC Q860RO;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY253271; AAC86775.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
SQ SEQUENCE 254 AA; 28588 MW; C81F2225D409AED2 CRC64;

Query Match 54.1%; Score 196; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.6e-180;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MAPRSLLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSD 60
Db      1  MAPRSLLISGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDDTQFLRFDSD 60
Qy      61  AAIPRMEPREPWEQEGQYWEWTTGYAKANAQTDVLRVLRNLLRRYNSAGSHTLQGMN 120
Db      61  AAIPRMEPREPWEQEGQYWEWTTGYAKANAQTDVLRVLRNLLRRYNSAGSHTLQGMN 120
Qy      121  GCDMGPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTY 180
Db      121  GCDMGPDGRLRGYHQHAYDGGKDYISLNEDLSRWTAADTVAQITQRFYEAEEYAEFFTY 180
Qy      181  LECECLELLRRYLENG 196
Db      181  LECECLELLRRYLENG 196

RESULT 8
Q8MGQI ID Q8MGQI PRELIMINARY; PRT; 346 AA.
AC Q8MGQI;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RA Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
 RN Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF523284; AAM74979.1; -;
 DR EMBL; AF523291; AAM74986.1; -;
 DR EMBL; AF523292; AAM74987.1; -;
 DR EMBL; AF645748; AAT73231.1; -;
 DR EMBL; AV645754; AAT73237.1; -;
 DR HSP; Q9TQHS; 1B0R.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHC_I; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; Igc1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;
 SQ
 Query Match 54.1%; Score 196; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2.1e-180; Indels 0; Gaps 0;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPRIAYEYVDDTQFLRFDS 60
 DB 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPRIAYEYVDDTQFLRFDS 60
 QY 61 AAIPRMEPREPWYEQEGPQYWEWTTGYAKANAQTDRLVALRNLRLRYNQEAGSHTLQGN 120
 DB 61 AAIPRMEPREPWYEQEGPQYWEWTTGYAKANAQTDRLVALRNLRLRYNQEAGSHTLQGN 120
 QY 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFPRTY 180
 DB 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFPRTY 180
 QY 181 LEGECLELLRRYLENG 196
 DB 181 LEGECLELLRRYLENG 196
 RESULT 9
 Q6DU20 PRELIMINARY; PRT; 346 AA.
 ID Q6DU20
 AC Q6DU20;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE MHC class Ib antigen.
 GN Name=HLA-F;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV645755; AAT73238.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; Cl-set; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; Igc1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;
 SQ
 Query Match 48.1%; Score 174; DB 2; Length 346;
 Best Local Similarity 99.6%; Pred. No. 3.7e-159; Indels 0; Gaps 0;
 Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 72 WVEQEGPQYWEWTTGYAKANAQTDRLVALRNLRLRYNQEAGSHTLQGMNGCDMPDGRLL 131
 DB 72 WVEQEGPQYWEWTTGYAKANAQTDRLVALRNLRLRYNQEAGSHTLQGMNGCDMPDGRLL 131
 QY 132 RGYHQHAYDGDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFPRTYLEGCELELLRR 191
 DB 132 RGYHQHAYDGDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFPRTYLEGCELELLRR 191
 QY 192 YLENGLETQRADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEETQDTEL 251
 DB 192 YLENGKETQRADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQRDGEETQDTEL 251
 QY 252 VETRPAGDGTFOKAAVAVVPSGEEQRYTCHVQHEGLPQPLLRWEQSPQPTIPIVIGVAG 311
 DB 252 VETRPAGDGTFOKAAVAVVPSGEEQRYTCHVQHEGLPQPLLRWEQSPQPTIPIVIGVAG 311
 QY 312 LVVLGAVVTGAVVAAMVMRKKSSDRNRGYSQA 346
 DB 312 LVVLGAVVTGAVVAAMVMRKKSSDRNRGYSQA 346
 RESULT 10
 Q6ZUW0 PRELIMINARY; PRT; 349 AA.
 ID Q6ZUW0
 AC Q6ZUW0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein FLJ43284.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahashi K., Masuho Y., Nagai K.,
 RA Isogai T.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK25274; BAC86108.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF07654; Cl-set; 1.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; Igc1; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Transmembrane.
 KW SEQUENCE 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;
 SQ

Query Match 40.9%; Score 148; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 4.9e-134; Indels 0; Gaps 0;
 Matches 148; Conservative 0; Mismatches 0;

QY 198 ETQRADPPKAVAHPIPSHAEATLRCWALGFYPAETTLTWRDGBEQOTDELVEVTPA 257
 DB 112 ETQRADPPKAVAHPIPSHAEATLRCWALGFYPAETTLTWRDGBEQOTDELVEVTPA 171

QY 258 GDCGTFKWAHVVPSEGEQRYTCHVQHEGLPQPLILRWESQPTPIVIGIVAGLVVLGA 317
 DB 172 GDCGTFKWAHVVPSEGEQRYTCHVQHEGLPQPLILRWESQPTPIVIGIVAGLVVLGA 231

QY 318 VVTGAVVAVMWRKSSDRNGYSQAA 345
 DB 232 VVTGAVVAVMWRKSSDRNGYSQAA 259

RESULT 11

1C28_PANTR STANDARD; PRT; 346 AA.
 AC P16215;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE CH1A class I histocompatibility antigen, CH28 alpha chain precursor.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90201944; PubMed=1690682;
 RA Lawlor D.A., Warren E., Ward F.E., Parham P.;
 RT "Comparison of class I MHC alleles in humans and apes.";
 RL Immunol. Rev. 113:147-185(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88319000; PubMed=3412487; DOI=10.1038/335268a0;
 RA Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.;
 RT "HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.";
 RL Nature 335:268-271(1988).
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
 CC -----
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 CC -----
 CC EMBL: M30685; AAA87973.1; --
 DR HSSP: Q29961; 1HSA.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC I; Signal; Transmembrane.
 FT SIGNAL 1 21
 FT CHAIN 22 346 CH1A class I histocompatibility antigen,
 FT DOMAIN 22 111 CH28 alpha chain.
 FT FT Extracellular alpha-1.

FT DOMAIN 112 203 Extracellular alpha-2.
 FT DOMAIN 204 295 Extracellular alpha-3.
 FT DOMAIN 296 329 Connecting peptide.
 FT TRANSMEM 306 329
 FT DOMAIN 330 346 Cytoplasmic tail.
 FT DISULFID 122 185 By similarity.
 FT DISULFID 224 280 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 346 AA; 39084 MW; F83B882D5C2E0971 CRC64;

Query Match 31.2%; Score 113; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.2e-100; Indels 0; Gaps 0;
 Matches 113; Conservative 0; Mismatches 0;

QY 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNVGMCDMPDGLRLRGYHQAHDGKD 143
 DB 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNVGMCDMPDGLRLRGYHQAHDGKD 143

QY 144 YISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGECLLELRRYLENG 196
 DB 144 YISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGECLLELRRYLENG 196

RESULT 12

Q95IT2 PRELIMINARY; PRT; 346 AA.
 AC Q95IT2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MHC class I antigen.
 GN Name=Patr-F;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21291697; PubMed=11398964; DOI=10.1007/s002510100318;
 RA Adams E.J., Parham P.;
 RT "Genomic analysis of common chimpanzee major histocompatibility complex class I genes.";
 RL Immunogenetics 53:200-208(2001).
 DR EMBL: AF338355; AAK77479.1; --
 DR HSSP: Q9TQHS; 1BOR.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF07654; C1-set; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGC1; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Transmembrane.
 SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 31.2%; Score 113; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.2e-100; Indels 0; Gaps 0;
 Matches 113; Conservative 0; Mismatches 0;

QY 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNVGMCDMPDGLRLRGYHQAHDGKD 143
 DB 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNVGMCDMPDGLRLRGYHQAHDGKD 143

QY 144 YISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGECLLELRRYLENG 196
 DB 144 YISLNEDLSWTAADTVAQITQRFYAEAYAEFFTYLEGECLLELRRYLENG 196

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RESULT 13
Q7YR27      PRELIMINARY;      PRT;      362 AA.
AC Q7YR27;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Class Ib.
GN Name=Patr-F;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]_TaxID=9598;
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Inanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
DR EMBL; AB100087; BAC78191.1; -.
DR HSSP; O9TQH5; 1B0R.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR010339; MHC I.
DR InterPro; IPR010579; MHC_I_C.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR Pfam; PF06623; MHC_I_C; 1.
DR ProDom; PD000050; MHC I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;

Query Match      31.2%; Score 113; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4e-100;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 TTGYAKANAQTDRLVALNRLNRRYNSAGSHTLQGNQCDMGDGLRLLRGYHQHAYDGD 143
DB 84 TTGYAKANAQTDRLVALNRLNRRYNSAGSHTLQGNQCDMGDGLRLLRGYHQHAYDGD 143

QY 144 YISLNEEDLSWTAADTVAQITQRFYEAEYAEFRYLEGECLELLRRYLENG 196
DB 144 YISLNEEDLSWTAADTVAQITQRFYEAEYAEFRYLEGECLELLRRYLENG 196

RESULT 14
Q9TPX7      PRELIMINARY;      PRT;      91 AA.
AC Q9TPX7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=Gogo-E;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]_TaxID=9593;
RP SEQUENCE FROM N.A.
KW Grimsley C.;

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF159566; AAD51614.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10354 MW; 2F485A66B6532A61 CRC64;

Query Match      24.0%; Score 87; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 PPKAHVAHPISDHEATLRCWALGYPFAEITLTWQRDGEQTDTELVTREPAGDTPQK 264
DB 1 PPKAHVAHPISDHEATLRCWALGYPFAEITLTWQRDGEQTDTELVTREPAGDTPQK 60

QY 265 WAAVVPSEGEQRYTCHVQHEGLPOPL 291
DB 61 WAAVVPSEGEQRYTCHVQHEGLPOPL 87

RESULT 15
Q29958      PRELIMINARY;      PRT;      316 AA.
AC Q29958;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE HLA-C protein (Fragment).
GN Name=HLA-C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=89122144; PubMed=2914713;
RA Cianetti L., Testa U., Scotto L., La Valle R., Simone A., Boccia G.,
RA Giannella G., Peschie C., Boncinelli E.;
RT "Three new class I HLA alleles: structure of mRNAs and alternative
RT mechanisms of processing.";
RL Immunogenetics 29:80-91 (1989).
DR EMBL; M24096; AAS59654.1; -.
DR PIR; C37028; C37028.
DR HSSP; Q9MY78; 1M05.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR010339; MHC I.
DR InterPro; IPR010579; MHC_I_C.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00129; MHC I; 1.
DR Pfam; PF06623; MHC_I_C; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35380 MW; C03B1EC87F75C9BA CRC64;

Query Match      20.2%; Score 73; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.3e-61;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	276	QRYTCHVQHEGLP	288
Db	229	QRYTCHVQHEGLP	241

Search completed: July 13, 2005, 09:11:49
Job time : 171 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:15:29 ; Search time 21.8528 Seconds
(without alignments)
935.984 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRYFSTAVSRPGRGP.....QRYTCHVQHGGLPQLILRW 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptcdat1/iaa/5A-COMB.pep.*
2: /cgn2_6/ptcdat1/iaa/5B-COMB.pep.*
3: /cgn2_6/ptcdat1/iaa/6A-COMB.pep.*
4: /cgn2_6/ptcdat1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptcdat1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptcdat1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	91.2	362	4	US-09-949-016-8242
2	29	36.1	120	4	US-09-513-999C-4290
3	44	16.1	274	1	US-08-222-851-1
4	43	15.7	358	4	US-09-949-016-6620
5	43	15.7	360	4	US-09-949-016-8370
6	39	14.2	117	2	US-08-406-057-9
7	39	14.2	117	2	US-08-958-316-9
8	39	14.2	145	2	US-08-406-057-8
9	39	14.2	145	3	US-08-958-316-8
10	39	14.2	338	4	US-09-949-016-6176
11	39	14.2	339	4	US-09-949-016-8636
12	30	10.9	289	2	US-08-484-905-79
13	30	10.9	289	3	US-08-481-985B-79
14	30	10.9	289	3	US-08-370-476-79
15	29	10.6	274	2	US-08-484-905-105
16	29	10.6	274	2	US-08-484-905-107
17	29	10.6	274	2	US-08-484-905-108
18	29	10.6	274	3	US-08-481-985B-105
19	29	10.6	274	3	US-08-481-985B-107
20	29	10.6	274	3	US-08-481-985B-108
21	29	10.6	274	3	US-08-370-476-105
22	29	10.6	274	3	US-08-370-476-107
23	29	10.6	274	3	US-08-370-476-108
24	29	10.6	341	3	US-08-890-719-38
25	29	10.6	365	2	US-08-484-905-97
26	29	10.6	365	2	US-08-484-905-98
27	29	10.6	365	2	US-08-484-905-99

28	29	10.6	365	2	US-08-484-905-100	Sequence 100, App
29	29	10.6	365	2	US-08-484-905-101	Sequence 101, App
30	29	10.6	365	3	US-08-481-985B-97	Sequence 97, Appl
31	29	10.6	365	3	US-08-481-985B-98	Sequence 98, Appl
32	29	10.6	365	3	US-08-481-985B-99	Sequence 99, Appl
33	29	10.6	365	3	US-08-481-985B-100	Sequence 100, App
34	29	10.6	365	3	US-08-481-985B-101	Sequence 101, App
35	29	10.6	365	3	US-08-652-265-23	Sequence 23, Appl
36	29	10.6	365	3	US-08-834-497A-23	Sequence 97, Appl
37	29	10.6	365	3	US-08-370-476-97	Sequence 98, Appl
38	29	10.6	365	3	US-08-370-476-98	Sequence 99, Appl
39	29	10.6	365	3	US-08-370-476-99	Sequence 100, App
40	29	10.6	365	3	US-08-370-476-100	Sequence 101, App
41	29	10.6	365	3	US-09-503-444A-23	Sequence 23, Appl
42	29	10.6	365	3	US-08-484-905-83	Sequence 83, Appl
43	27	9.9	184	2	US-08-481-985B-83	Sequence 83, Appl
44	27	9.9	184	3	US-08-370-476-83	Sequence 83, Appl
45	27	9.9	184	3	US-08-370-476-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-8242
; Sequence 8242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 8242
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8242

Query Match 91.2%; Score 250; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 9.3e-240;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGPRIAYEVYDDTFLRFDSDAATPRMSPREPWEQGPQYW 60
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Db 22 GSHSLRYFSTAVSRPGRGPRIAYEVYDDTFLRFDSDAATPRMSPREPWEQGPQYW 81
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QY 61 EWTGTYAKANAQTDRVALNLLRRYRNQSEAGSHTLQGMNCGMDGPDGRLLRGYHQHAYDG 120
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Db 82 EWTGTYAKANAQTDRVALNLLRRYRNQSEAGSHTLQGMNCGMDGPDGRLLRGYHQHAYDG 141
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QY 121 KQYISLNEDLRSWTAADTVAQITQRYEAEFEVYAEPRTYLEGCECLLRRLRYLNGKETLQ 180
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Db 142 KQYISLNEDLRSWTAADTVAQITQRYEAEFEVYAEPRTYLEGCECLLRRLRYLNGKETLQ 201
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QY 181 RADPPKAAVHAHPISDHEATLRCWALGFYPAETITLWQRDGEQOTDTLVEVTRPADGDT 240
|||||
Db 202 RADPPKAAVHAHPISDHEATLRCWALGFYPAETITLWQRDGEQOTDTLVEVTRPADGDT 261
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QY 241 FQKWAADVVP 250
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Db 262 FQKWAADVVP 271
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RESULT 2
US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLLLLSGALALT/DT
US-09-513-999C-4290

Query Match          36.1%; Score 99; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 99; Conservative 0;

QY 1 GSHSLRYSTAVSRGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPREPWVQEGPOYW 60
DB 22 GSHSLRYSTAVSRGRGEPRIAYVYDDTQFLRFDSDAAIPRMEPREPWVQEGPOYW 81

QY 61 EWTGYAKANAQTRVALNRLRRYNSQAGSHTLQGMN 99
DB 82 EWTGYAKANAQTRVALNRLRRYNSQAGSHTLQGMN 120

RESULT 3
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKI, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:

US-09-949-016-6620
; Sequence 949-016-6620
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6620
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6620

Query Match          15.7%; Score 43; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 2e-34; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0;

QY 225 TQDTVELVETRPAGDGTFOKWAADVVPSEGEQRYTCHVQHEGLP 267
DB 246 TQDTVELVETRPAGDGTFOKWAADVVPSEGEQRYTCHVQHEGLP 288

RESULT 5
US-09-949-016-8370
; Sequence 8370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 8370
LENGTH: 360
TYPE: PRT
ORGANISM: Human
US-09-949-016-8370

Query Match 15.7% Score 43; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 2e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 225 TQDELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 267
DB 248 TQDELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 290

RESULT 6

US-08-406-057-9
Sequence 9, Application US/08406057
Patent No. 5856442
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-057-9

Query Match 14.2% Score 39; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 51 ELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 89

RESULT 7

US-08-958-316-9
Sequence 9, Application US/08958316
Patent No. 6291659
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-958-316-9

Query Match 14.2% Score 39; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 ELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 267
DB 51 ELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 89

RESULT 8
US-08-406-057-8
Sequence 8, Application US/08406057
Patent No. 5856442
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA

COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.2e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267
|||||
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117
|||||

RESULT 9
US-08-958-316-8
Sequence 8, Application US/08958316
Patent No. 6291659
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: GLUCKMAN, ELIANE
APPLICANT: KIRSZENBAUM, MAKEK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSES: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-958-316-8

Query Match 14.2%; Score 39; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.2e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267
|||||
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117
|||||

RESULT 10
US-09-949-016-6176
Sequence 6176, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6176
LENGTH: 338
TYPE: PRT
ORGANISM: Human
US-09-949-016-6176

Query Match 14.2%; Score 39; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267
|||||
DB 253 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291
|||||

RESULT 11
US-09-949-016-8636
Sequence 8636, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 8636
;; LENGTH: 339
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-8636

Query Match 14.2%; Score 39; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 ELVETRPAGDGTQKWAHVVPSEGEQRYTCHVQHEGLP 267
Db 254 ELVETRPAGDGTQKWAHVVPSEGEQRYTCHVQHEGLP 292

RESULT 12
US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 QDTELVTETRPAGDGTQKWAHVVPSEGEQ 255
Db 226 QDTELVTETRPAGDGTQKWAHVVPSEGEQ 255

RESULT 13
US-08-481-985B-79
; Sequence 79, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-985B-79

Query Match 10.9%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 226 QDTELVTETRPAGDGTQKWAHVVPSEGEQ 255
Db 226 QDTELVTETRPAGDGTQKWAHVVPSEGEQ 255

RESULT 14
US-08-370-476-79
; Sequence 79, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe

```

RESULT 15
US-08-484-905-105
; Sequence 105, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Etelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700

```

```

1 CITY: Washington
2 STATE: D.C.
3 ZIP: 20005-3315
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy Disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: PatentIn Release #1.0, Version #1.25
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/484,905
11 FILING DATE: 07-JUNE-1995
12 CLASSIFICATION: 530
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/801,818
15 FILING DATE: 05-DEC-1991
16 CLASSIFICATION: 530
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/792,473
19 FILING DATE: 15-NOV-1991
20 CLASSIFICATION: 530
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Potter, Jane E. R.
23 REGISTRATION NUMBER: 33,332
24 REFERENCE/DOCKET NUMBER: 03495.0106-03000
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 202-408-4000
27 TELEFAX: 202-408-4400
28 INFORMATION FOR SEQ ID NO: 105:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 274 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 US-08-484-905-105
35
36 Query Match 10.6%; Score 29; DB 2; Length 274;
37 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
38 Matches 29; Conservative 0; Mismatches 0; Indels
39
40 QY 224 QTQDTVELVETRPAGDGTQKWAIVVPSG 252
41
42 Db 224 QTQDTVELVETRPAGDGTQKWAIVVPSG 252
43
44 Search completed: July 13, 2005, 09:29:09
45 Job time : 22.8528 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:02:43 ; Search time 40 Seconds
(without alignments)
870.762 Million cell updates/sec

Title: US-09-819-371-4
Perfect score: 362
Sequence: 1 MAPRSLLLSGALATDTW.....QAAVTSAGSGVSLTANKV 362

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	261	72.1	362	2 A60384	MHC class I histoc
2	113	31.2	345	2 S07114	MHC class I histoc
3	73	20.2	316	2 C37028	MHC class I histoc
4	59	16.3	348	2 S29390	histocompatibility
5	44	12.2	275	1 HLH010	MHC class I histoc
6	44	12.2	298	2 S44994	class I histocompa
7	44	12.2	313	2 I36958	MHC class I histoc
8	44	12.2	325	2 I54449	MHC class I HLA-Cx
9	44	12.2	332	2 S06424	MHC class I histoc
10	44	12.2	345	2 I68749	MHC class I lympho
11	44	12.2	354	2 I54551	histocompatibility
12	44	12.2	357	2 I36966	MHC class I protei
13	44	12.2	357	2 I36965	MHC class I protei
14	44	12.2	359	1 HLH012	MHC class I histoc
15	44	12.2	364	2 S03535	class I histocompa
16	44	12.2	365	2 S01171	class I histocompa
17	44	12.2	365	2 I36961	MHC class I protei
18	44	12.2	365	2 I37476	MHC class I histoc
19	44	12.2	365	2 A47636	MHC class I histoc
20	44	12.2	365	2 I83063	All-2 - human
21	44	12.2	365	2 I56039	HLA-A30.3 precurs
22	44	12.2	365	2 I61856	MHC class I histoc
23	44	12.2	365	2 I37478	MHC class I histoc
24	44	12.2	365	2 I54493	MHC class I histoc
25	44	12.2	365	2 S77963	MHC class I histoc
26	44	12.2	365	2 I38519	MHC class I histoc
27	44	12.2	365	2 I54416	HLA-AW24 protein -
28	44	12.2	365	2 I38518	HLA-A-0102 allele
29	44	12.2	366	1 HLH0W3	MHC class I histoc

ALIGNMENTS

RESULT 1

A60384

MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60384; JI0147
R;Lury, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-537, 1990

A;Title: The human class I MHC gene HLA-F is expressed in lymphocytes.

A;Reference number: A60384; MUID:91197889; PMID:1707659

A;Accession: A60384

A;Molecule type: DNA

A;Residues: 1-362 <EUR>

A;Cross-references: UNIPROT:P30511

R;Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.

J. Exp. Med. 171, 1-18, 1990

A;Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I

A;Reference number: JI0147; MUID:90111605; PMID:1688605

A;Accession: JI0147

A;Molecule type: DNA

A;Residues: 1-362 <GER>

A;Cross-references: GB:X17093; NID:G32223; PIDN:CAA34947.1; PID:G312407

A;Experimental source: lymphoblastoid cell line

C;Genetics:

A;Gene: GDB:HLA-F

A;Cross-references: GDB:125714

A;Map position: 6p21.3-6p21.3

A;Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: glycoprotein; heterodimer; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-111/Domain: alpha-1 <ALL>

F;78-104/Region: hypervariable

F;112-203/Domain: alpha-2 <AL2>

F;164-192/Region: hypervariable

F;204-295/Domain: alpha-3 <AL3>

F;217-282/Domain: immunoglobulin homology <IMM>

F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.1%; Score 261; DB 2; Length 362;

Best Local Similarity 99.7%; Pred. No. 8.1e-249;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPRSLLLSGALATDTWAGSHSLRYSTAVSRGCEPRYIAVEYDDTQFLRPDSD 60

DB 1 MAPRSLLLSGALATDTWAGSHSLRYSTAVSRGCEPRYIAVEYDDTQFLRPDSD 60

QY 61 AAIPTREPEPWVEQGPQYEWTTGYAKANAQTDVALNLRNLRNRRNQSEAGSHTLQGMN 120

DB 61 AAIPTREPEPWVEQGPQYEWTTGYAKANAQTDVALNLRNLRNRRNQSEAGSHTLQGMN 120

QY 121 GCDMGDPGRLRLRGYHQHAYDKGYISLNEDLSRWSWTAADTVQAQITQRFYEAEBEFTY 180

Db 121 GCDMGPDGRLRGYHQHAYDGDGYISLNEEDLSWTAADTAQITQRFYEAEYAEFFTY 180
QY 181 LEQCELELLRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240
Db 181 LEQCELELLRRYLENGKETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240
QY 241 DGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLPQPLILRWEQSPQ 300
Db 241 DGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLPQPLILRWEQSPQ 300
QY 301 PTPIPIVIGIAGLVGLVAVVTGAVAAVMWRKSSDRNGSSQAAVTSQAQSGVSLTAN 360
Db 301 PTPIPIVIGIAGLVGLVAVVTGAVAAVMWRKSSDRNGSSQAAVTSQAQSGVSLTAN 360
QY 361 KV 362
Db 361 KV 362

RESULT 2

S07114
MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S07114
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A:Reference number: S06424; MUID:88319000; PMID:3412487
A:Accession: S07114

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-345 <LAW>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: Glycoprotein; membrane protein
F:217-282/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 113; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-103;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 TTGYAKANAQTRVALNRLRRYNOSEAGSHYTLQNGCDMGPDGRLRGYHQHAYDGD 143
Db 84 TTGYAKANAQTRVALNRLRRYNOSEAGSHYTLQNGCDMGPDGRLRGYHQHAYDGD 143

QY 144 YISLNEEDLSWTAADTAQITQRFYEAEYAEFFTYLEGECELELLRRYLENG 196
Db 144 YISLNEEDLSWTAADTAQITQRFYEAEYAEFFTYLEGECELELLRRYLENG 196

RESULT 3

C37028
MHC class I histocompatibility antigen HLA-C (clone 9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: C37028
R:Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella
Immunogenetics 29, 80-91, 1989
A:Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of
A:Reference number: A37028; MUID:89122144; PMID:2914713
A:Accession: C37028

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-316 <CIA>
A:Cross-references: UNIPROT:Q96F05; UNIPROT:Q29987; UNIPROT:Q9MY34; UNIPROT:O19677; UNIP
C:Genetics:
A:Gene: GDB:HLA-C
A:Cross-references: GDB:119311; OMIM:142840
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:170-235/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 73; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.1e-63;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 216 SDHEATLRCWALGFYPAEITLTWORDBGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEE 275
Db 169 SDHEATLRCWALGFYPAEITLTWORDBGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEE 228
QY 276 QRYTCHVQHEGLP 288
Db 229 QRYTCHVQHEGLP 241

RESULT 4

S29990
histocompatibility antigen, HLA-F-like - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S29990

R:Bontrop, R.R.
submitted to the EMBL Data Library, February 1993

A:Reference number: S29990
A:Accession: S29990
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BON>
A:Cross-references: UNIPROT:P33617; EMBL:221819; NID:G38569; PIDN:CAA79885.1; PID:G38569
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:219-284/Domain: immunoglobulin homology <IMM>

Query Match 16.3%; Score 59; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.3e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 233 EITLTWORDBGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLPQPL 291
Db 235 EITLTWORDBGEQOTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLPQPL 293

RESULT 5

HLH10
MHC class I histocompatibility antigen HLA-A10 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: B24512

R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.

J. Biol. Chem. 260, 13414-13423, 1985

A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A:Reference number: A92500; MUID:86033791; PMID:3863816

A:Accession: B24512

A:Molecule type: DNA

A:Residues: 1-275 <DAV>

A:Cross-references: UNIPROT:P01892; GB:M11887; NID:G184157; PIDN:AAA52656.1; PID:G184157

C:Genetics:

A:Gene: GDB:HLA-A

A:Cross-references: GDB:119310; OMIM:142800

A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

F:130-195/Domain: immunoglobulin homology <IMM>

F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.2%; Score 44; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLP 288
Db 158 QTQDTLQVETRPAGDGTTFQKAAVVVPVSGEQRVYCHVOHEGLP 201

RESULT 6

S44994

class I histocompatibility antigen HLA-Cw6 precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S44994
R:Margot, M.; Brockstedt, D.; Jenisch, S.
submitted to the EMBL Data Library, May 1994
A:Description: New HLA-Cw6 sequence.
A:Reference number: S44994
A:Accession: S44994
A:Molecule type: mRNA
A:Residues: 1-298 <MAR>
A:Cross-references: UNIPROT:Q29866; EMBL:Z33459; NID:g488361; PID:g488361
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:1-72/Domain: signal sequence #status predicted <SIG>
F:73-298/Product: class I histocompatibility antigen HLA-Cw6 (fragment) #status predicted
F:220-285/Domain: immunoglobulin homology <IM>

Query Match 12.2%; Score 44; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.8e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288
|||||
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 291
|||||

RESULT 7

I36958
MHC class I - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I36958
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215; PMID:2715640
A:Accession: I36958
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <RES>
A:Cross-references: UNIPROT:Q30989; GB:M24046; NID:g176816; PID:AAA3425.1; PID:g176817
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:167-232/Domain: immunoglobulin homology <IM>

Query Match 12.2%; Score 44; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 4e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288
|||||
DB 195 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 238
|||||

RESULT 8

I54449
MHC class I HLA-Cx52 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jan-2000
C:Accession: I54449
R:Takata, H.; Inoko, H.; Ando, A.; Haranaka, M.; Watanabe, B.; Tsuji, K.; Iri, H.
Immunogenetics 28, 265-270, 1988
A:Title: Cloning and analysis of HLA class I cDNA encoding a new HLA-C specificity Cx52.
A:Reference number: I54449; MUID:88330144; PMID:2843461
A:Accession: I54449
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-325 <RES>
A:Cross-references: GB:M21963; NID:g188540; PID:AAA59847.1; PID:g188541
C:Genetics:
A:Gene: GDB:HLA-C
A:Cross-references: GDB:119311; OMIM:142840
A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:179-244/Domain: immunoglobulin homology <IM>

Query Match 12.2%; Score 44; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288
|||||
DB 207 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 250
|||||

RESULT 9

S06424
MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee
N:Alternate names: MHC Ch1a chain
C:Species: Pan troglodytes (chimpanzee)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S06424; I36959
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A:Reference number: S06424; MUID:88319000; PMID:3412487
A:Accession: S06424
A:Molecule type: mRNA
A:Residues: 1-332 <LAW>
A:Cross-references: UNIPROT:Q30990
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A:Title: Diversity and diversification of HLA-A,B,C alleles.
A:Reference number: I36956; MUID:89235215; PMID:2715640
A:Accession: I36959
A:Molecule type: mRNA
A:Residues: 1-332 <RES>
A:Cross-references: GB:M24047; NID:g176818; PID:AAA35426.1; PID:g553155
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-114/Domain: alpha-1 #status predicted <EX1>
F:115-206/Domain: alpha-2 #status predicted <EX2>
F:220-285/Domain: immunoglobulin homology <IM>
F:307-331/Domain: transmembrane #status predicted <TM>
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:125-188,227-283/Disulfide bonds: #status predicted

Query Match 12.2%; Score 44; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.2e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288
|||||
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 291
|||||

RESULT 10

I68749
MHC class I lymphocyte antigen - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I68749
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B
A:Reference number: I54457; MUID:89233295; PMID:2714852
A:Accession: I68749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: UNIPROT:Q29963; GB:M28206; NID:g576476; PID:AAA57258.1; PID:g57647
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:199-264/Domain: immunoglobulin homology <IM>

Query Match 12.2%; Score 44; DB 2; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
Db 227 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 270
|||||

RESULT 11
I54551
histocompatibility antigen - crab-eating macaque (fragment)
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54551
R:Boyson, J.E.; McAdam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes, Immunogenetics 41, 59-68, 1995
A:Title: The MHC E locus in macaques is polymorphic and is conserved between macaques and
A:Reference number: I54551; MUID:95104933; PMID:7806297
A:Accession: I54551
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: UNIPROT:Q95513; EMBL:U02976; NID:g413827; PIDN:AAA70050.1; PID:g4138
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:209-274/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 354;
Best Local Similarity 100.0%; Pred. No. 4.4e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
Db 237 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 280
|||||

RESULT 12
I36966
MHC class I protein - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: I36966
R:Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I. Immunogenetics 38, 238-240, 1993
A:Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.
A:Reference number: I36965; MUID:93279743; PMID:8505066
A:Accession: I36966
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-357 <RES>
A:Cross-references: UNIPROT:Q9MXL2; UNIPROT:Q30993; GB:M55245; NID:g176836; PIDN:AAA0368
C:Genetics:
A:Gene: A6
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 4.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
Db 240 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 283
|||||

RESULT 13
I36965
MHC class I protein (A5) - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I36965
R:Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I. Immunogenetics 38, 238-240, 1993
A:Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.

A:Reference number: I36965; MUID:93279743; PMID:8505066
A:Accession: I36965
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-357 <RES>
A:Cross-references: UNIPROT:Q9MXL1; UNIPROT:Q30992; GB:M55244; NID:g176834; PIDN:AAA7206
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:212-277/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 4.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
Db 240 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 283
|||||

RESULT 14
HLHUI2
MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4) - hu
C:Species: Homo sapiens (man)
C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C:Accession: A02189
R:Malissen, M.; Malissen, B.; Jordan, B.R. Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A:Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A:Reference number: A02189; MUID:82151002; PMID:6461010
A:Accession: A02189
A:Molecule type: DNA
A:Residues: 1-359 <NAL>
A:Cross-references: GB:J00191; GB:V00526; NID:g187600; PIDN:AAA36218.1; PID:g386873
C:Comment: The seven exons correspond approximately to the domain structure of this chain.
C:Genetics:
A:Map position: 6p21.3
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted <
F:22-304/Domain: extracellular #status predicted <EXT>
F:22-111/Domain: alpha-1 <EX1>
F:112-203/Domain: alpha-2 <EX2>
F:217-282/Domain: immunoglobulin homology <IMM>
F:305-329/Domain: transmembrane #status predicted <TMM>
F:335-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted

Query Match 12.2%; Score 44; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
Db 245 QTQDTLVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||

RESULT 15
S03535
class I histocompatibility antigen ChLA-A108 alpha chain precursor - chimpanzee (fragmen
C:Species: Pan troglodytes (chimpanzee)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
C:Accession: S03535
R:Mayer, W.B.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, G.; Klein, J. EMBO J. 7, 2765-2774, 1988
A:Title: Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-spec
A:Reference number: S01171; MUID:89030641; PMID:2460344
A:Accession: S03535
A:Molecule type: mRNA
A:Residues: 1-364 <MAY>
A:Cross-references: UNIPROT:P13748; EMBL:X13113; NID:g38212; PIDN:CAA31505.1; PID:g7557
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: transmembrane protein

C;Keywords: transmembrane protein
F;1-23/Domain: signal sequence (fragment) #status predicted <SIG>
F;24-364/Product: Class I histocompatibility antigen alpha chain #status predicted <MAT>
F;24-297/Domain: extracellular #status predicted <EXT>
F;219-284/Domain: immunoglobulin homology <IMM>
F;298-336/Domain: transmembrane #status predicted <TMH>
F;297-364/Domain: intracellular #status predicted <INT>

Query Match

Query Match 12.2%; Score 44; DB 2; L
Best Local Similarity 100.0%; Pred. No. 4.6e-35;

BEST LOCAL SIMILARITY 100.0%; FREQ. NO. 4.6E-35;
 MATCHES 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 QTQDTLVEVTRPAGDGTQKWAAVVVPSSGEEQRYTCHVQHEGLP 288

Db 247 QTQDTLTVETRPAGDGTFOKWAAVVPSGEEQRYTCHVQHEGLP 290

Search completed: July 13, 2005, 09:15:25

Job time : 41 secs

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OM protein - protein search, using sw model.

Run on: July 13, 2005, 09:25:40 ; Search time 120.47 Seconds
(without alignments)
878.681 Million cell updates/sec

Title: US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRYFSTAVSRPGRGEP.....QRYTCHVQHGLPQPLILRW 274

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	11 US-09-819-371-5	Sequence 5, Appli
2	274	100.0	362	15 US-10-257-021-82	Sequence 82, Appl
3	274	100.0	422	16 US-10-408-765A-1887	Sequence 1887, Ap
4	241	88.0	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	63.9	362	11 US-09-819-371-4	Sequence 4, Appli
6	119	43.4	215	11 US-09-819-371-6	Sequence 6, Appli
7	70	25.5	186	15 US-10-264-049-4063	Sequence 4063, Ap
8	68	24.8	96	14 US-10-029-386-30718	Sequence 30718, A
9	44	16.1	77	14 US-10-029-386-34273	Sequence 34273, A
10	44	16.1	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	16.1	104	9 US-09-925-302-835	Sequence 835, App

12	44	16.1	104	10 US-09-925-302-835	Sequence 835, App
13	44	16.1	365	17 US-10-741-600-941	Sequence 941, App
14	43	15.7	476	16 US-10-430-984-16	Sequence 16, Appl
15	43	15.7	500	16 US-10-430-984-15	Sequence 15, Appl
16	40	14.6	78	14 US-10-029-386-30752	Sequence 30752, A
17	40	14.6	371	15 US-10-085-198-72	Sequence 72, Appl
18	40	14.6	371	15 US-10-210-172-156	Sequence 156, App
19	39	14.2	91	9 US-09-864-761-38005	Sequence 38005, A
20	39	14.2	92	15 US-10-380-880-5	Sequence 5, Appli
21	39	14.2	169	16 US-10-741-601-383	Sequence 383, App
22	39	14.2	169	17 US-10-741-601-1135	Sequence 1135, Ap
23	39	14.2	198	16 US-10-741-601-387	Sequence 387, App
24	39	14.2	198	17 US-10-741-600-1143	Sequence 1143, Ap
25	39	14.2	234	15 US-10-380-880-8	Sequence 8, Appli
26	39	14.2	251	16 US-10-741-601-384	Sequence 384, App
27	39	14.2	251	17 US-10-741-600-1142	Sequence 1142, Ap
28	39	14.2	284	15 US-10-104-047-3648	Sequence 3648, Ap
29	39	14.2	326	15 US-10-380-880-7	Sequence 7, Appli
30	39	14.2	338	16 US-10-741-601-380	Sequence 380, App
31	39	14.2	338	16 US-10-741-601-388	Sequence 388, App
32	39	14.2	338	17 US-10-741-600-1134	Sequence 1134, Ap
33	39	14.2	338	17 US-10-741-600-1138	Sequence 1138, Ap
34	39	14.2	338	17 US-10-482-029-110	Sequence 110, App
35	39	14.2	343	16 US-10-741-601-379	Sequence 379, App
36	39	14.2	343	17 US-10-741-600-1139	Sequence 1139, Ap
37	39	14.2	379	15 US-10-093-463-78	Sequence 78, Appl
38	39	14.2	379	15 US-10-210-172-160	Sequence 160, App
39	38	13.9	145	9 US-09-810-560-8	Sequence 8, Appli
40	36	13.1	45	14 US-10-029-386-28883	Sequence 28883, A
41	32	11.7	91	9 US-09-864-761-35461	Sequence 35461, A
42	32	11.7	110	9 US-09-796-692-799	Sequence 799, App
43	32	11.7	110	9 US-09-796-692-2139	Sequence 2139, Ap
44	32	11.7	110	14 US-10-040-862-799	Sequence 799, App
45	32	11.7	110	14 US-10-040-862-2139	Sequence 2139, Ap

ALIGNMENTS

RESULT 1

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca
; FILE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match	100.0%	Score	274	DB	11	Length	274
Best Local Similarity	100.0%	Pred. No.	2.4e-260				
Matches	274	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	GSHSLRYFSTAVSRPGRGEPRIAYVVDQTLRFSDAAIPRMEPREPWQEGPQYW	60				
Db	1	GSHSLRYFSTAVSRPGRGEPRIAYVVDQTLRFSDAAIPRMEPREPWQEGPQYW	60				
QY	61	EWTTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQGMNGCDMPDGRLLRGYHAYDG	120				
Db	61	EWTTGYAKANAQTDRLVALNLLRRYNSQSGSHTLQGMNGCDMPDGRLLRGYHAYDG	120				
QY	121	KDYISLNEDLRSWTAADTVAQITQRFYEAEVAAEFRTYLEGECLELLRRYLENGKETLQ	180				
Db	121	KDYISLNEDLRSWTAADTVAQITQRFYEAEVAAEFRTYLEGECLELLRRYLENGKETLQ	180				

Db 148 KDVISLNEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGCELELLRRYLENGKETLQ 207
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPABEITLTWQRDGEQTDTELVEPTRAGDGT 240
Db 208 RADPPKARVAHPISDHEATLRCWALGFYPABEITLTWQRDGEQTDTELVEPTRAGDGT 267
QY 241 F 241
Db 268 F 268

RESULT 5
US-09-819-371-4
; Sequence 4, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

Query Match 63.9%; Score 175; DB 11; Length 362;
Best Local Similarity 100.0%; Pred. No. 5e-163;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSHSLRYFSTAVSRPGRGEPRIYAVEVDDTQFLRFDSDAAIPRMEPRPWPVQEGPOYM 60
Db 22 GSHSLRYFSTAVSRPGRGEPRIYAVEVDDTQFLRFDSDAAIPRMEPRPWPVQEGPOYM 81
QY 61 EWTGKAKANAQTRDVALRNLRRYNQSEAGSHTLQMGNCMDGPDGRLRLRGYHQHAYDG 120
Db 82 EWTGKAKANAQTRDVALRNLRRYNQSEAGSHTLQMGNCMDGPDGRLRLRGYHQHAYDG 141
QY 121 KDVISLNEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGCELELLRRYLENG 175
Db 142 KDVISLNEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGCELELLRRYLENG 196

RESULT 6
US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 43.4%; Score 119; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119 DGKDYISLNEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGCELELLRRYLENGKET 178
Db 97 DGKDYISLNEDLRSWTAADTVAQITQRFYAEYAEFFTYLEGCELELLRRYLENGKET 156

QY 179 LQADPPKARVAHPISDHEATLRCWALGFYPABEITLTWQRDGEQTDTELVEPTRAG 237
Db 157 LQADPPKARVAHPISDHEATLRCWALGFYPABEITLTWQRDGEQTDTELVEPTRAG 215
RESULT 7
US-10-264-049-4063
; Sequence 4063, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4063
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (148)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (176)

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; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4063

Query Match      25.5%; Score 70; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YAKANAQTRVALNLLRRYNOSEAGSHTLQGNCGDMGPDGRLLRGVHGHAYDGGKDYIS 125
Db 1 YAKANAQTRVALNLLRRYNOSEAGSHTLQGNCGDMGPDGRLLRGVHGHAYDGGKDYIS 60
QY 126 LNEDLRSWTA 135
Db 61 LNEDLRSWTA 70

RESULT 8
US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

Query Match      24.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 DPPKAHVAAHPISDHEATLRCWALGFPYPAEITLTWQDGEQQTQDTLTVETRPAGDGTGQ 242
Db 2 DPPKAHVAAHPISDHEATLRCWALGFPYPAEITLTWQDGEQQTQDTLTVETRPAGDGTGQ 61
QY 243 KWAAVVVP 250
Db 62 KWAAVVVP 69

RESULT 9
US-10-029-386-34273
; Sequence 34273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34273
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273

Query Match      16.1%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.4e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVVPSPGSEORYTCHVQHEGLP 267
Db 25 QTQDTLTVETRPAGDGTGFKWAAVVVPSPGSEORYTCHVQHEGLP 68

RESULT 10
US-10-029-386-31089
; Sequence 31089, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31089
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004204.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52
US-10-029-386-31089

Query Match      16.1%; Score 44; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.3e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLTVETRPAGDGTGFKWAAVVVPSPGSEORYTCHVQHEGLP 267
Db 41 QTQDTLTVETRPAGDGTGFKWAAVVVPSPGSEORYTCHVQHEGLP 84

RESULT 11
US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 835

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (95)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match

Best Local Similarity 16.1%; Score 44; DB 9; Length 104;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 32 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 12

US-09-925-302-835

; Sequence 835, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 835

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (95)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match

Best Local Similarity 16.1%; Score 44; DB 10; Length 104;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 32 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 13

US-10-741-600-941

; Sequence 941, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 941

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-600-941

Query Match

Best Local Similarity 16.1%; Score 44; DB 17; Length 365;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 248 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 14

US-10-430-984-16

; Sequence 16, Application US/10430984

; Publication No. US20040225112A1

; GENERAL INFORMATION:

; APPLICANT: The Board of Trustees of the University of Arkansas

; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)

; FILE REFERENCE: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity

; CURRENT APPLICATION NUMBER: US/10/430,984

; CURRENT FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 476

; TYPE: PRT

; ORGANISM: human leukocyte antigen E-Single chain dimer

US-10-430-984-16

Query Match

Best Local Similarity 15.7%; Score 43; DB 16; Length 476;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 364 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 406

RESULT 15

US-10-430-984-15

; Sequence 15, Application US/10430984

; Publication No. US20040225112A1

; GENERAL INFORMATION:

; APPLICANT: The Board of Trustees of the University of Arkansas

; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)

; FILE REFERENCE: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity

; CURRENT APPLICATION NUMBER: US/10/430,984

; CURRENT FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 15

; LENGTH: 500

; TYPE: PRT

; ORGANISM: human leukocyte antigen E-Single chain Trimer

US-10-430-984-15

Query Match

Best Local Similarity 15.7%; Score 43; DB 16; Length 500;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 388 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 430

Search completed: July 13, 2005, 09:46:00

Job time : 121.47 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:09:04 ; Search time 43 Seconds
(without alignments)
628.441 Million cell updates/sec

Title: US-09-819-371-4
Perfect score: 362
Sequence: 1 MAPRSLLLSGALALTDWT.....QAATVDSAGSGVSLTANKV 362

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	196	54.1	362	4	US-09-949-016-8242
2	120	33.1	120	4	US-09-513-999C-4290
3	44	12.2	274	1	US-08-222-851-1
4	43	11.9	358	4	US-09-949-016-6620
5	43	11.9	360	4	US-09-949-016-8370
6	39	10.8	117	2	US-08-406-057-9
7	39	10.8	117	3	US-08-958-316-9
8	39	10.8	145	2	US-08-406-057-8
9	39	10.8	145	3	US-08-958-316-8
10	39	10.8	338	4	US-09-949-016-6176
11	39	10.8	339	4	US-09-949-016-8636
12	30	8.3	289	2	US-08-484-905-79
13	30	8.3	289	3	US-08-481-985B-79
14	30	8.3	289	3	US-08-370-476-79
15	29	8.0	274	2	US-08-484-905-105
16	29	8.0	274	2	US-08-484-905-107
17	29	8.0	274	2	US-08-484-905-108
18	29	8.0	274	3	US-08-481-985B-105
19	29	8.0	274	3	US-08-481-985B-107
20	29	8.0	274	3	US-08-481-985B-108
21	29	8.0	274	3	US-08-370-476-105
22	29	8.0	274	3	US-08-370-476-107
23	29	8.0	274	3	US-08-370-476-108
24	29	8.0	341	3	US-08-890-719-38
25	29	8.0	365	2	US-08-484-905-97
26	29	8.0	365	2	US-08-484-905-98
27	29	8.0	365	2	US-08-484-905-99

28	29	8.0	365	2	US-08-484-905-100	Sequence 100, App
29	29	8.0	365	2	US-08-484-905-101	Sequence 101, App
30	29	8.0	365	3	US-08-481-985B-97	Sequence 97, Appl
31	29	8.0	365	3	US-08-481-985B-98	Sequence 98, Appl
32	29	8.0	365	3	US-08-481-985B-99	Sequence 99, Appl
33	29	8.0	365	3	US-08-481-985B-100	Sequence 100, App
34	29	8.0	365	3	US-08-481-985B-101	Sequence 101, App
35	29	8.0	365	3	US-08-652-265-23	Sequence 23, Appl
36	29	8.0	365	3	US-08-834-497A-23	Sequence 23, Appl
37	29	8.0	365	3	US-08-370-476-97	Sequence 97, Appl
38	29	8.0	365	3	US-08-370-476-98	Sequence 98, Appl
39	29	8.0	365	3	US-08-370-476-99	Sequence 99, Appl
40	29	8.0	365	3	US-08-370-476-100	Sequence 100, App
41	29	8.0	365	3	US-08-370-476-101	Sequence 101, App
42	29	8.0	365	3	US-09-503-444A-23	Sequence 23, Appl
43	27	7.5	184	2	US-08-484-905-83	Sequence 83, Appl
44	27	7.5	184	3	US-08-481-985B-83	Sequence 83, Appl
45	27	7.5	184	3	US-08-370-476-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-8242
; Sequence 8242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8242
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8242

Query Match	54.1%	Score 196;	DB 4;	Length 362;
Best Local Similarity	100.0%;	Pred. No. 9.5e-178;		
Matches 196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAPRSLLLSGALALTDWTAGSHSLRYSTAVSRGCRGPXYIAVEYVDDTQFLRFDSD	60	
Db	1	MAPRSLLLSGALALTDWTAGSHSLRYSTAVSRGCRGPXYIAVEYVDDTQFLRFDSD	60	
Qy	61	AALPRMEPRPWEQSGPQYWEWTGKAKANAQTDVRLNLLRRYNSAGSHHTLOGMN	120	
Db	61	AALPRMEPRPWEQSGPQYWEWTGKAKANAQTDVRLNLLRRYNSAGSHHTLOGMN	120	
Qy	121	GCDMGPDGRLRLRYHQHAYDGDYISLNEDLRSWTAAATVAQITQRPYAEVEAEPRTY	180	
Db	121	GCDMGPDGRLRLRYHQHAYDGDYISLNEDLRSWTAAATVAQITQRPYAEVEAEPRTY	180	
Qy	181	LEGECELLRRYLENG	196	
Db	181	LEGECELLRRYLENG	196	

RESULT 2
US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961

```
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLILLSSGALMT/DT
US-09-513-999C-4290

Query Match      33.1%; Score 120; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.7e-106; Mismatches 0; Indels 0; Gaps 0;
Matches 120; Conservative 0;

QY 1 MAPRSLLLSGALMTDTWAGSHSLRYSTAVSRGRGEPRIAYEVYDDTQFLRFSD 60
    |||||||
Db 1 MAPRSLLLSGALMTDTWAGSHSLRYSTAVSRGRGEPRIAYEVYDDTQFLRFSD 60
    |||||||

QY 61 AAIPRMEPPEVQSGPYQWMTTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGN 120
    |||||||
Db 61 AAIPRMEPPEVQSGPYQWMTTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGN 120
    |||||||

RESULT 3
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKY, ALAN M.
; APPLICANT: FARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28600-20200.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRNFOERSH
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-1

Query Match      12.2%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTGKAAVAVVPSGEEQRYTCHVQHEGLP 288
    |||||||
Db 224 QTQDTLVELTRPAGDGTGKAAVAVVPSGEEQRYTCHVQHEGLP 267
    |||||||

RESULT 4
US-09-949-016-6620
; Sequence 6620, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6620
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6620

Query Match      11.9%; Score 43; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 TQDTELVELTRPAGDGTGKAAVAVVPSGEEQRYTCHVQHEGLP 288
    |||||||
Db 246 TQDTELVELTRPAGDGTGKAAVAVVPSGEEQRYTCHVQHEGLP 288
    |||||||

RESULT 5
US-09-949-016-8370
; Sequence 8370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8370
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Human
```


COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-331-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-057-8

Query Match 10.8%; Score 39; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117
|||||

RESULT 9
US-09-819-371-4
; Sequence 8, Application US/08958316
; Patent No. 6291659
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-958-316-8

Query Match 10.8%; Score 39; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.3e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117
|||||

RESULT 10
US-09-949-016-6176
; Sequence 6176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6176
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6176

Query Match 10.8%; Score 39; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 9.7e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
|||||
DB 253 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291
|||||

RESULT 11
US-09-949-016-8636
; Sequence 8636, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8636
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8636

Query Match 10.8%; Score 39; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 9.7e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 288
|||||

DB 254 ELVETRPAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 292
|||||

RESULT 12

US-08-484-905-79
; Sequence 79, Application US/08484905
; Patent No. 5976551

GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-484-905-79

Query Match 8.3%; Score 30; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDTELVEPRAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 276
|||||

DB 226 QDTELVEPRAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 255
|||||

RESULT 13

US-08-481-985B-79
; Sequence 79, Application US/08481985B
; Patent No. 6011146

GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-481-985B-79

Query Match 8.3%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDTELVEPRAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 276
|||||

DB 226 QDTELVEPRAGDGTQKWAADVVPSEGEORVYCHVQHEGLP 255
|||||

RESULT 14

US-08-370-476-79
; Sequence 79, Application US/08370476
; Patent No. 6153408

GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Casrouge, Armanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex

;;
;; TITLE OF INVENTION:
;; NUMBER OF SEQUENCES: 127
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; ZIP: 20005-3315
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/370,476
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/117,575
;; FILING DATE: 07-SEP-1993
;; APPLICATION NUMBER: US 08/072,787
;; FILING DATE: 06-JUN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/801,818
;; FILING DATE: 05-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/792,473
;; FILING DATE: 15-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 05243.0001-01000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 79:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 289 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-08-370-476-79

Query Match 8.3%; Score 30; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDTLVETRPAGDGTFOKWAAVVPSGERQ 276
|||
Db 226 QDTLVETRPAGDGTFOKWAAVVPSGERQ 255

RESULT 15
US-08-484-905-105
; Sequence 105, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Morte, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:

;;
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,905
;; FILING DATE: 07-JUNE-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/801,818
;; FILING DATE: 05-DEC-1991
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/792,473
;; FILING DATE: 15-NOV-1991
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E. R.
;; REGISTRATION NUMBER: 33,332
;; REFERENCE/DOCKET NUMBER: 03495.0106-03000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 105:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 274 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-08-484-905-105

Query Match 8.0%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QDTLVETRPAGDGTFOKWAAVVPSG 273
|||
Db 224 QDTLVETRPAGDGTFOKWAAVVPSG 252

Search completed: July 13, 2005, 09:24:23
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:14:49 ; Search time 163 Seconds
(without alignments)
857.989 Million cell updates/sec

Title: US-09-819-371-4
Perfect score: 362
Sequence: 1 MAPRSLLLSGALALTDW.....QAATDSAGSGVSLTANKV 362

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpaa/PCT05_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	362	100.0	362	11 US-09-819-371-4	Sequence 4, Appli
2	261	72.1	362	15 US-10-257-021-82	Sequence 82, Appl
3	244	67.4	442	16 US-10-408-765A-1887	Sequence 1887, Ap
4	196	54.1	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	48.3	274	11 US-09-819-371-5	Sequence 5, Appli
6	95	26.2	215	11 US-09-819-371-6	Sequence 6, Appli
7	70	19.3	186	15 US-10-264-049-4063	Sequence 4063, Ap
8	68	18.8	96	14 US-10-029-386-30718	Sequence 30718, Ap
9	44	12.2	77	14 US-10-029-386-34273	Sequence 34273, A
10	44	12.2	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	12.2	104	9 US-09-925-302-835	Sequence 835, App

12	44	12.2	104	10 US-09-925-302-835	Sequence 835, App
13	44	12.2	365	17 US-10-741-600-941	Sequence 941, App
14	43	11.9	476	16 US-10-430-984-16	Sequence 16, Appl
15	43	11.9	500	16 US-10-430-984-15	Sequence 15, Appl
16	40	11.0	78	14 US-10-029-386-30752	Sequence 30752, A
17	40	11.0	371	15 US-10-085-198-72	Sequence 72, Appl
18	40	11.0	371	15 US-10-210-172-156	Sequence 156, App
19	39	10.8	91	9 US-09-864-761-38005	Sequence 38005, A
20	39	10.8	92	15 US-10-380-880-5	Sequence 5, Appli
21	39	10.8	169	16 US-10-741-601-383	Sequence 383, App
22	39	10.8	169	17 US-10-741-600-1135	Sequence 1135, Ap
23	39	10.8	198	16 US-10-741-601-387	Sequence 387, App
24	39	10.8	198	17 US-10-741-600-1143	Sequence 1143, Ap
25	39	10.8	234	15 US-10-380-880-8	Sequence 8, Appli
26	39	10.8	251	16 US-10-741-601-384	Sequence 384, App
27	39	10.8	251	17 US-10-741-600-1142	Sequence 1142, Ap
28	39	10.8	284	15 US-10-104-047-3648	Sequence 3648, Ap
29	39	10.8	326	15 US-10-380-880-7	Sequence 7, Appli
30	39	10.8	338	16 US-10-741-601-380	Sequence 380, App
31	39	10.8	338	16 US-10-741-601-388	Sequence 388, App
32	39	10.8	338	17 US-10-741-600-1134	Sequence 1134, Ap
33	39	10.8	338	17 US-10-741-600-1138	Sequence 1138, Ap
34	39	10.8	338	17 US-10-482-029-110	Sequence 110, App
35	39	10.8	343	16 US-10-741-601-379	Sequence 379, App
36	39	10.8	343	17 US-10-741-600-1139	Sequence 1139, Ap
37	39	10.8	379	15 US-10-093-463-78	Sequence 78, Appl
38	39	10.8	379	15 US-10-210-172-160	Sequence 160, App
39	38	10.5	145	9 US-09-810-560-8	Sequence 8, Appli
40	36	9.9	45	14 US-10-029-386-28883	Sequence 28883, A
41	32	8.8	91	9 US-09-864-761-35461	Sequence 35461, A
42	32	8.8	110	9 US-09-796-692-799	Sequence 799, App
43	32	8.8	110	9 US-09-796-692-2139	Sequence 2139, Ap
44	32	8.8	110	14 US-10-040-862-799	Sequence 799, App
45	32	8.8	110	14 US-10-040-862-2139	Sequence 2139, Ap

ALIGNMENTS

RESULT 1

US-09-819-371-4
; Sequence 4, Application US/09819371
; Publication No. US2004005344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-4

Query Match 100.0%; Score 362; DB 11; Length 362;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGPGEPRIYAVYVDDTQFLRFS	60
Db	1	MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGPGEPRIYAVYVDDTQFLRFS	60
QY	61	AAIPRMEPRPVEGEGQYWEWTTGYAKANAQTRVALNLLRRYNQSEAGSHTLQGN	120
Db	61	AAIPRMEPRPVEGEGQYWEWTTGYAKANAQTRVALNLLRRYNQSEAGSHTLQGN	120
QY	121	GCDMGPDGRLRGYHQHAYDGDYISLNEDSLRSWTAADTVAQITQRFYAEYAEFRFY	180
Db	121	GCDMGPDGRLRGYHQHAYDGDYISLNEDSLRSWTAADTVAQITQRFYAEYAEFRFY	180

QY 181 LECELELLRRYLENGLETQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQR 240
Db |||||
QY 241 DGEETQDTLVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Db |||||
QY 301 PTPIVIGIVAGLVVLGAVVTGAVAAVMWRKSSDRNRGYSQAAVTDQAQSGVSLTAN 360
Db |||||
QY 361 KV 362
Db |||||

Auto-mated

RESULT 2
US-10-257-021-82
; Sequence 82, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.036902
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-021-82

Query Match 72.1%; Score 261; DB 15; Length 362;
Best Local Similarity 99.7%; Pred. No. 1e-233;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRFSD 60
Db |||||
QY 61 AAPRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALRNLLRRYNQSEAGSHTLQGMN 120
Db |||||
QY 121 GCDMGPDGRLRGYHQAHDGKDYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFRY 180
Db |||||
QY 181 LECELELLRRYLENGLETQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQR 240
Db |||||
QY 241 DGEETQDTLVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Db |||||
QY 301 PTPIVIGIVAGLVVLGAVVTGAVAAVMWRKSSDRNRGYSQAAVTDQAQSGVSLTAN 360
Db |||||
QY 361 KV 362
Db |||||

Db 361 KV 362
RESULT 3
US-10-408-765A-1887
; Sequence 1887, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1887
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1887
Query Match 67.4%; Score 244; DB 16; Length 442;
Best Local Similarity 99.7%; Pred. No. 7.6e-218;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRFSD 60
Db |||||
QY 61 AAPRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALRNLLRRYNQSEAGSHTLQGMN 120
Db |||||
QY 121 GCDMGPDGRLRGYHQAHDGKDYISLNEDLSRSTAADTVAQITQRFYEAEEYAEFRY 180
Db |||||
QY 181 LECELELLRRYLENGLETQADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQR 240
Db |||||
QY 241 DGEETQDTLVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Db |||||
QY 301 PTPIVIGIVAGLVVLGAVVTGAVAAVMWRKSSDRNRGYSQAA 345
Db |||||

RESULT 4
US-09-925-301-1431
; Sequence 1431, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431

Query Match 54.1%; Score 196; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 2e-173;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRSLLLSGALALDTWAGSHSLRYFSTAVSRPGRPRIYAVEYVDDTQFLRFDSD 60
DB 7 MAPRSLLLSGALALDTWAGSHSLRYFSTAVSRPGRPRIYAVEYVDDTQFLRFDSD 66

QY 61 AAIIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQGMN 120
DB 67 AAIIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQGMN 126

QY 121 GCDMGPDGRLRLRGYHQHAYDGKDYISLNEDLSRWTAADTVAQITQRYEAEYAEPRTY 180
DB 127 GCDMGPDGRLRLRGYHQHAYDGKDYISLNEDLSRWTAADTVAQITQRYEAEYAEPRTY 186

QY 181 LEGECLELLRRYLENG 196
DB 187 LEGECLELLRRYLENG 202

RESULT 5

US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-5

Query Match 48.3%; Score 175; DB 11; Length 274;
Best Local Similarity 100.0%; Pred. No. 6.6e-154;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GSHSLRYFSTAVSRPGRPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 81
DB 1 GSHSLRYFSTAVSRPGRPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYW 60

QY 82 EWTGTGAKANAQTDVALNLLRRYNSAGSHTLQGMNGCDMGPDGRLRLRGYHQHAYDG 141
DB 61 EWTGTGAKANAQTDVALNLLRRYNSAGSHTLQGMNGCDMGPDGRLRLRGYHQHAYDG 120

QY 142 KDYISLNEDLSRWTAADTVAQITQRYEAEYAEPRTYLEGECLELLRRYLENG 196
DB 121 KDYISLNEDLSRWTAADTVAQITQRYEAEYAEPRTYLEGECLELLRRYLENG 175

RESULT 6

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/819,371

; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

Query Match 26.2%; Score 95; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDVALNLL 103
DB 1 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDVALNLL 60

QY 104 RRYNSQSEAGSHTLQGMNGCDMGPDGRLRLRGYHQHA 138
DB 61 RRYNSQSEAGSHTLQGMNGCDMGPDGRLRLRGYHQHA 95

RESULT 7

US-10-264-049-4063
; Sequence 4063, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4063
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (148)

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; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (176)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4063

Query Match      19.3%; Score 70; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 YAKANAQTRVALRNLRRYNQSEAGSHTLQMGNGDMPDGLLRGVHGHAYDKGYIS 146
      |||||||
Db      1 YAKANAQTRVALRNLRRYNQSEAGSHTLQMGNGDMPDGLLRGVHGHAYDKGYIS 60

QY      147 LNEDLRSWTA 156
      |||||||
Db      61 LNEDLRSWTA 70

RESULT 8
US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

Query Match      18.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      204 DPPKAHVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 263
      |||||||
Db      2 DPPKAHVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 61

QY      264 KWAAVVVP 271
      |||||||
Db      62 KWAAVVVP 69

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (176)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4063

Query Match      19.3%; Score 70; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      87 YAKANAQTRVALRNLRRYNQSEAGSHTLQMGNGDMPDGLLRGVHGHAYDKGYIS 146
      |||||||
Db      1 YAKANAQTRVALRNLRRYNQSEAGSHTLQMGNGDMPDGLLRGVHGHAYDKGYIS 60

QY      147 LNEDLRSWTA 156
      |||||||
Db      61 LNEDLRSWTA 70

RESULT 8
US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

Query Match      18.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 7e-55;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      204 DPPKAHVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 263
      |||||||
Db      2 DPPKAHVAHPHPSDHEATLRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 61

QY      264 KWAAVVVP 271
      |||||||
Db      62 KWAAVVVP 69
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RESULT 9
US-10-029-386-34273
; Sequence 34273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34273
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273

Query Match      12.2%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 288
      |||||||
Db      25 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 68

RESULT 10
US-10-029-386-31089
; Sequence 31089, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31089
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004204.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52
US-10-029-386-31089

Query Match      12.2%; Score 44; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 288
      |||||||
Db      41 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 84
```

RESULT 11

US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 835
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match

12.2%; Score 44; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

245 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 288
|||||

Db

32 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 75
|||||

RESULT 12

US-09-925-302-835
; Sequence 835, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 835
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match

12.2%; Score 44; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

245 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 288
|||||

Db

32 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 75
|||||

RESULT 13

US-10-741-600-941

; Sequence 941, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 941
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-941

Query Match 12.2%; Score 44; DB 17; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.6e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

245 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 288
|||||

Db

248 QTQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 291
|||||

RESULT 14

US-10-430-984-16
; Sequence 16, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: Crew, Mark D
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
; TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
; FILE REFERENCE: 8793-53098
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 476
; TYPE: PRT
; ORGANISM: human leukocyte antigen E-Single chain dimer
US-10-430-984-16

Query Match 11.9%; Score 43; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 5e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

246 TQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 288
|||||

Db

364 TQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 406
|||||

RESULT 15

US-10-430-984-15
; Sequence 15, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: Crew, Mark D
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
; TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
; FILE REFERENCE: 8793-53098
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: human leukocyte antigen E-Single chain Trimer
US-10-430-984-15

Query Match 11.9%; Score 43; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 5e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

246 TQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 288
|||||

Db

364 TQDTLVETRPAGDGTFOKAAVVPVPSGEEQRYTCHVQHEGLP 406
|||||

Search completed: July 13, 2005, 09:28:24
Job time : 164 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:59:16 ; Search time 164 Seconds
(without alignments)
853.703 Million cell updates/sec

Title: US-09-819-371-4
Perfect score: 362
Sequence: 1 MAPRSLLLSGALATDTW.....QAAVTDSAGQGVSLTANKV 362

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	362	4	AAG64617 Human can
2	261	72.1	362	4	ABBS0296 HLA-Cw ov
3	261	72.1	362	7	ADFS5587 Human can
4	261	72.1	362	8	ADJ75372 Marker ge
5	261	72.1	362	8	ADP12500 Protein e
6	261	72.1	362	8	ABM80784 Tumour-as
7	261	72.1	362	8	ADP23768 PRO polyp
8	261	72.1	362	8	ADP23768 PRO polyp
9	244	67.4	442	7	ADJ70081 Human can
10	196	54.1	271	3	ABM80784 Human can
11	196	54.1	677	4	ABG26726 Novel hum
12	175	48.3	274	4	AAG64618 Human can
13	175	48.3	274	7	ADFS5588 Fragment
14	153	42.3	215	4	AAG64619 Human can
15	153	42.3	215	7	ADFS5589 Fragment
16	148	40.9	349	8	ADQ65964 Novel hum
17	120	33.1	120	3	AAG00209 Human sec
18	74	20.4	120	7	ADI21206 Novel hum
19	70	19.3	186	5	ABP42931 Human ova
20	68	18.8	96	8	ABO57084 Human gen
21	44	12.2	77	8	ABO60639 Human gen
22	44	12.2	91	8	ABO57455 Human gen
23	44	12.2	104	3	ABBS58497 Lung can
24	44	12.2	274	1	AAP80911 Consensus
25	44	12.2	365	8	ADP12521 Protein e

26	44	12.2	365	8	ADQ39278	Adq39278 Human myo
27	44	12.2	366	2	AAR12466	Aar12466 HLA-C exo
28	44	12.2	366	2	AAY07033	Aay07033 Breast ca
29	44	12.2	366	7	ADI62997	Adi62997 Human apo
30	44	12.2	366	7	ADP65326	Adp65326 Human HLA
31	44	12.2	366	7	ADP65316	Adp65316 Human hla
32	44	12.2	366	8	ADP65316	Adp65316 Human hla
33	44	12.2	366	8	ADP65316	Adp65316 Human hla
34	44	12.2	366	8	ADP65316	Adp65316 Human hla
35	44	12.2	366	8	ADP65316	Adp65316 Human hla
36	44	12.2	366	8	ADP65316	Adp65316 Human hla
37	43	11.9	120	4	AAU32883	Aau32883 Novel hum
38	43	11.9	120	4	AAU32883	Aau32883 Novel hum
39	43	11.9	120	4	AAU32883	Aau32883 Novel hum
40	43	11.9	120	4	AAU32883	Aau32883 Novel hum
41	40	11.0	187	8	ADP29434	Adp29434 Human sec
42	40	11.0	187	8	ADP29434	Adp29434 Human sec
43	40	11.0	187	8	ADP29434	Adp29434 Human sec
44	40	11.0	187	8	ADP29434	Adp29434 Human sec
45	40	11.0	187	8	ADP29434	Adp29434 Human sec

ALIGNMENTS

RESULT 1
AAG64617
ID AAG64617 standard; protein; 362 AA.

AC AAG64617;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human cancer cell specific HLA-F antigen SEQ ID 4.
XX
KW HLA-F antigen; cancer cell specific; human.
XX
OS Homo sapiens.

PN JP2001095584-A.
XX
PD 10-APR-2001.
XX
PF 30-SEP-1999; 99JP-00279566.
XX
PR 30-SEP-1999; 99JP-00279566.
XX
PS (EGAW/) EGAWA K.
PA (MEDI-) MEDINET KK.
PA (KIMU/) KIMURA K.

DR WPI; 2001-360493/38.
DR N-PSDB; AAH45555.
XX
FT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
XX
PS Disclosure; Page 9-10; 12pp; Japanese.
XX
CC This invention relates to a cancer cell specific HLA-F antigen. The
CC invention includes DNA encoding the antigen, and a method for the
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
CC invention

XX
SQ Sequence 362 AA;
Query Match 72.1%; Score 261; DB 4; Length 362;
Best Local Similarity 99.7%; Pred. No. 1.4e-229;
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPRSLLLSGALATDTWAGSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRPDS 60

Db 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYDDTQFLRFDS 60
Qy 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDVALNLLRRYNNQSEAGSHTLQGMN 120
Db 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDVALNLLRRYNNQSEAGSHTLQGMN 120
Qy 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFFRY 180
Db 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFFRY 180
Qy 181 LECECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240
Db 181 LECECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240
Qy 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Db 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Qy 301 PTPIPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360
Db 301 PTPIPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360
Qy 361 KV 362
Db 361 KV 362

RESULT 2

ABB50296
ID ABB50296 standard; protein; 362 AA.

XX
AC ABB50296;

XX
DT 08-FEB-2002 (first entry)

XX
DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

XX
KW Ovarian tumour marker gene; human; overexpression; upregulation;
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localised; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine.

XX
OS Homo sapiens.

XX
PN WO200175177-A2.

XX
XX 11-OCT-2001.

XX
PF 03-APR-2001; 2001WO-US010947.

XX
PR 03-APR-2000; 2000US-0194336P.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX
DR WPI: 2001-626450/72.

XX
DR N-PSDB; ABA83122.

XX
PT Detecting and identifying ovarian tumor, identifying increased risk for
PT developing ovarian cancer, and determining effectiveness of ovarian
PT cancer treatment, by measuring expression level of ovarian tumor marker
PT gene.

XX
PS Claim 23; Page 126-127; 140pp; English.

XX

CC The invention relates to methods for diagnosing and prognosing ovarian
CC tumours in an individual via the detection and measurement of the
CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
CC ABA83181 and ABA83183). The methods of the invention are useful for
CC detecting an ovarian tumour in a patient, for identifying an individual
CC at increased risk for developing ovarian cancer, in prognostic tests for
CC assessing the relative severity of ovarian cancer, in tests for
CC monitoring a patient in remission from ovarian cancer and in tests for
CC monitoring disease status in a patient being treated for ovarian cancer.
CC The methods can additionally be used to identify a particular tumour as
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from
CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
CC mucinous cystadenoma, borderline mucinous tumour, mucinous
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
CC tumour. The ovarian tumour marker genes of the invention were identified
CC using SAGE (serial analysis of gene expression) and were found to be
CC overexpressed in a broad variety of ovarian epithelial tumour cells
CC relative to normal ovarian epithelial cells. The marker genes are
CC implicated in immune response pathways, in the regulation of cell
CC proliferation and in protein folding, and many of these are membrane-
CC localised or secreted. In addition to their use as diagnostic and
CC prognostic markers, the ovarian tumour marker genes of their encoded
CC proteins may be used as therapeutic targets for the treatment and
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent
CC proteins encoded by ovarian tumour marker genes of the invention
XX
SQ Sequence 362 AA;

Query Match 72.1%; Score 261; DB 4; Length 362;
Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYDDTQFLRFDS 60
Db 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYDDTQFLRFDS 60

Qy 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDVALNLLRRYNNQSEAGSHTLQGMN 120
Db 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDVALNLLRRYNNQSEAGSHTLQGMN 120

Qy 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFFRY 180
Db 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFFRY 180

Qy 181 LECECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240
Db 181 LECECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240

Qy 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300
Db 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQPLILRWEQSPQ 300

Qy 301 PTPIPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360
Db 301 PTPIPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360

Qy 361 KV 362
Db 361 KV 362

RESULT 3
ADF55587

XX ID ADF55587 standard; protein; 362 AA.

XX AC ADF55587;

XX DT 12-FEB-2004 (first entry)

XX DE Human cancer-cell specific HLA-F antigen.

XX

Matches	361;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	MAPRSLLLLSGALALTD	TWAGSHSLRYFSTAVSRPGRGEP	RYIAVEVYDDTQFLRFDSD	60				
DB	1	MAPRSLLLLSGALALTD	TWAGSHSLRYFSTAVSRPGRGEP	RYIAVEVYDDTQFLRFDSD	60				
QY	61	AAIPRMPREPWEQEGPQ	WVETTTGYAKANAQTD	VALRNLRLRYN	OSEAGSHTLQGMN	120			
DB	61	AAIPRMPREPWEQEGPQ	WVETTTGYAKANAQTD	VALRNLRLRYN	OSEAGSHTLQGMN	120			
QY	121	GCDMGPGRLRGVGH	QYHAYDKDYISLNED	LSRWSWTAADT	VQAQITQRFYEA	EYAEFEFTY	180		
DB	121	GCDMGPGRLRGVGH	QYHAYDKDYISLNED	LSRWSWTAADT	VQAQITQRFYEA	EYAEFEFTY	180		
QY	181	LEGCELLRLRYLENG	LETQLRADPPKAAV	HAHPISDHEAT	LRCLWALGFYPA	ITLWQ	240		
DB	181	LEGCELLRLRYLENG	LETQLRADPPKAAV	HAHPISDHEAT	LRCLWALGFYPA	ITLWQ	240		
QY	241	DGEETQDTVELT	ETRPAGDGTFOKAA	VVVVPSGEEQRYT	CHVQHEGLPQL	LILRWEQSPQ	300		
DB	241	DGEETQDTVELT	ETRPAGDGTFOKAA	VVVVPSGEEQRYT	CHVQHEGLPQL	LILRWEQSPQ	300		
QY	301	PTIPIVGIVAGLV	GLAVTGVAVVA	VMWRKSSDRNRGS	YSQAAVTD	SAQSGVSLTAN	360		
DB	301	PTIPIVGIVAGLV	GLAVTGVAVVA	VMWRKSSDRNRGS	YSQAAVTD	SAQSGVSLTAN	360		
QY	361	KV	362						
DB	361	KV	362						
RESULT 5									
ID	ADP12500	standard; protein; 362 AA.							
XX	AC	ADP12500;							
XX	DT	12-AUG-2004 (first entry)							
XX	XX	Protein encoded by mRNA of the invention #110.							
DE	XX	transplant rejection; immune system; rheumatoid arthritis; lupus;							
XX	KW	inflammatory bowel disease; multiple sclerosis; HIV; AIDS.							
KW	KW	Homo sapiens.							
OS	XX	WO2004042346-A2.							
XX	PN	21-MAY-2004.							
XX	PD	24-APR-2003; 2003WO-US012946.							
PF	XX	24-APR-2002; 2002US-00131831.							
XX	PR	20-DEC-2002; 2002US-00325899.							
XX	PP	(EXPR-) EXPRESSION DIAGNOSTICS INC.							
XX	PA	Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;							
XX	PI	Rosenberg S;							
XX	PI	WPI; 2004-400724/37.							
XX	DR	Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,							
PPT	PPT	pancreas, pancreatic islet, lung, bone marrow or stem cell transplant							
PPT	PPT	rejection, in an individual, comprises detecting the expression level of							
PPT	PPT	the genes.							
XX	XX	Claim 65; SEQ ID NO 2509; 1762pp; English.							
XX	XX	The present invention relates to diagnosing or monitoring transplant							
CC	CC	rejection, e.g. cardiac or kidney transplant rejection, in an individual							
CC	CC	comprises detecting the expression level of one or more genes. The							
CC	CC	methods, system and kits are useful in diagnosing or monitoring							

transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.

Sequence 362 AA;

Query Match 72.1%; Score 261; DB 8; Length 362;
Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Qy		1	M A P R S L L L L S G A L A L T D T W A G S H S L R Y F S T A V S R P G E P R Y I A V E Y V D D T Q F L R F O S D	60
Db		1	M A P R S L L L L S G A L A L T D T W A G S H S L R Y F S T A V S R P G E P R Y I A V E Y V D D T Q F L R F O S D	60
Qy		61	A A I P R M E P R E P W E O E G P Q W E W T T G Y A K A N A Q T D R V A L R N L L R R Y N O S E A G S H T L O G N N	120
Db		61	A A I P R M E P R E P W E O E G P Q W E W T T G Y A K A N A Q T D R V A L R N L L R R Y N O S E A G S H T L O G N N	120
Qy		121	G C D M G P D R L L R G Y H O H A Y D G K O Y I S L N E D L R S W T A A D T V A Q I T O R F Y E A E Y A E E F R T Y	180
Db		121	G C D M G P D R L L R G Y H O H A Y D G K O Y I S L N E D L R S W T A A D T V A Q I T O R F Y E A E Y A E E F R T Y	180
Qy		181	L E G E C L E L L R R Y L E N G X E T L Q R A D P P K A H V A H P I S D H E A T L R C W A L G F Y P A E I T L T W O R	240
Db		181	L E G E C L E L L R R Y L E N G X E T L Q R A D P P K A H V A H P I S D H E A T L R C W A L G F Y P A E I T L T W O R	240
Qy		241	D G S E O Q D T L E V T R P A G D G T F Q K W A A V V P S G S E Q R Y T C H V O H E G L P O P L I L R W E Q S P Q	300
Db		241	D G S E O Q D T L E V T R P A G D G T F Q K W A A V V P S G S E Q R Y T C H V O H E G L P O P L I L R W E Q S P Q	300
Qy		301	P T T I P I V G I A G L V V L G A V V T G A V V A A V W M R K K S D R N R G S Y S Q A A V T D S A Q G S G Y S L T A N	360
Db		301	P T T I P I V G I A G L V V L G A V V T G A V V A A V W M R K K S D R N R G S Y S Q A A V T D S A Q G S G Y S L T A N	360
Qy		361	K V 362	
Db		361	K V 362	

RESIT.T 6

ABM80784	
ID	ABM80784 standard; protein; 362 AA.
XX	
XX	
AC	ABM80784;
XX	
DT	18-NOV-2004 (first entry)
DE	
DE	Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018
XX	
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW	central nervous system cancer; bladder cancer; pancreatic cancer;
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;
KW	chromosome identification; chromosome mapping; gene mapping;
KW	gene therapy; cytostatic.
XX	
OS	Homo sapiens.
XX	
XX	WO2004030615-A2.
XX	
XX	
PD	15-APR-2004.
XX	
PF	29-SEP-2003; 2003WO-US028547.
XX	
XX	
PR	02-OCT-2002; 2002US-0414971P.
XX	

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

DR N-PSDB; ACN38477.

XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 2018; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX Sequence 362 AA;

Query Match 72.1%; Score 261; DB 8; Length 362;

Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60

Db 1 MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60

Qy 61 AAPRMEPREPWVEQEPQYWEWTTGYAKANAQTDVVALNRLNRRYNSAGSHTLQGMN 120

Db 61 AAPRMEPREPWVEQEPQYWEWTTGYAKANAQTDVVALNRLNRRYNSAGSHTLQGMN 120

Qy 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLRSGWTAADTVAQITQRYEAEYAEPRTY 180

Db 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLRSGWTAADTVAQITQRYEAEYAEPRTY 180

Qy 181 LEGECLELLRRLYENGLTQLRADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240

Db 181 LEGECLELLRRLYENGLTQLRADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240

Qy 241 DGEEOQDTLVELTRPAGDGTFCQKAAVVPVSGEEQRYTCHVQHEGLPQLILRWESQP 300

Db 241 DGEEOQDTLVELTRPAGDGTFCQKAAVVPVSGEEQRYTCHVQHEGLPQLILRWESQP 300

Qy 301 PTPIVGIVAGLVGLVAVVTGAVVAAVWWRKKSDDNRNGYSQAQVTDSSAQSGSVSLTAN 360

Db 301 PTPIVGIVAGLVGLVAVVTGAVVAAVWWRKKSDDNRNGYSQAQVTDSSAQSGSVSLTAN 360

Qy 361 KV 362

Db 361 KV 362

RESULT 7

ADP23768

ID ADP23768 standard; protein; 362 AA.

XX

AC ADP23768;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:946.

DE

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;

KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;

KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

OS

XX WO2004041170-A2.

PN

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

PF

XX 01-NOV-2002; 2002US-0423394P.

PR

XX (GETH) GENENTECH INC.

XX

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;

PI Wu TD;

XX WPI; 2004-419628/39.

DR N-PSDB; ADP23767.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated

PT renal disease, or demyelinating diseases of the central or peripheral

PT nervous system.

XX Claim 7; SEQ ID NO 946; 2940pp; English.

XX

XX The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has

CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the

CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous

CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary

CC disease, infectious or autoimmune chronic active hepatitis, primary

CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food

CC hypersensitivity, urticaria, an immunologic disease of the lung,

CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

CC pneumonitis, a transplantation associated disease, graft rejection or

CC graft-versus-host disease. The present sequence represents a PRO protein

CC of the invention.

XX Sequence 362 AA;

Qy Query Match 72.1%; Score 261; DB 8; Length 362;

Db Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60

Db 1 MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60

QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNV 120
 Db |||||
 QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNV 120
 Db |||||
 QY 121 GCDMPDGRLLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180
 Db |||||
 QY 121 GCDMPDGRLLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180
 QY 181 LECECLELRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240
 Db |||||
 QY 181 LECECLELRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240
 QY 241 DGEEOQTDELVELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300
 Db |||||
 QY 301 PTPIPIVIGIAGLVGLGAVVTGAVAAVMWRKSSDRNGSYSQAAVTDASQSGVSLTAN 360
 Db |||||
 QY 361 KV 362
 Db |||||

RESULT 8

ADSF74309
 ID ADSF74309 standard; protein; 362 AA.

XX AC ADSF74309;

XX 16-DEC-2004 (first entry)

XX PRO polypeptide PRO81414, role in immune-related disease.

XX PRO81414; psoriasis; ulcerative colitis; gastrointestinal-gen.;

KW antipsoriatic; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..17

FT Protein /label= Signal_peptide

FT Protein /label= Mature_protein

FT Region 22..200

FT Modified-site /note= "Class I histocompatibility antigen"

FT Modified-site 107..110

FT Modified-site 118..123

FT Region 131..136

FT Modified-site /note= "N-glycosylation site"

FT Modified-site /note= "N-myristoylation site"

FT Modified-site /note= "Crystallins beta and gamma 'Greek key' motif signature"

FT Domain /notes= "Tyrosine kinase phosphorylation site"

FT Region /label= Immunoglobulin

FT Domain /note= "Immunoglobulins and major histocompatibility complex proteins signature"

FT Modified-site /label= Transmembrane

FT Modified-site 307..312

FT Modified-site 316..321

FT Modified-site 321..326

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 330..333

FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 331..334
 FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
 FT Modified-site 352..357
 FT /note= "N-myristoylation site"
 FT Modified-site 354..359
 FT /note= "N-myristoylation site"
 FT Region 360..362
 FT /note= "Microbodies C-terminal targeting signal"

XX WO2004081199-A2.

PN 23-SEP-2004.

XX 10-MAR-2004; 2004WO-US007862.

XX 11-MAR-2003; 2003US-0454025P.

XX (GETH) GENENTECH INC.

XX Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;

XX WPI: 2004-668955/65.

XX N-PSDB; ADS74308.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and

XX treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid

XX arthritis.

XX Claim 9; SEQ ID NO 28; 166pp; English.

XX The present sequence is the protein sequence of novel human PRO

XX polypeptide PRO81414. The invention provides newly identified and

XX isolated nucleotide sequences encoding polypeptides referred to as PRO

XX polypeptides that are useful in the diagnosis and treatment of immune-

XX related diseases. Microarray analysis showed that expression of PRO81414

XX is up-regulated 1.2-fold in lesional skin as compared to non-lesional

XX skin from psoriasis patients and up-regulated 1.5-fold in colon samples

XX from ulcerative colitis patients as compared to normal colon. It is also

XX down-regulated 2-fold upon differentiation of monocytes into macrophages

XX after 7 days in differentiation media and up-regulated 4-fold in

XX dendritic cells upon activation with LPS. PRO81414 can be used in a

XX claimed method of identifying a compound that inhibits expression of the

XX gene encoding it. The candidate compound is especially an antisense

XX nucleic acid. The PRO polypeptide can be obtained by recombinant

XX expression, especially in CHO, Escherichia coli or yeast host cells. The

XX polypeptide, its antagonist or an antibody that binds the polypeptide are

XX used in claimed methods for the alleviation or diagnosis of psoriasis and

XX ulcerative colitis.

XX Sequence 362 AA;

XX Query Match 72.1%; Score 261; DB 8; Length 362;

XX Best Local Similarity 99.7%; Pred No. 1.4e-229;

XX Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSD 60

Db |||||

QY 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPYIAVEYVDDTQFLRFDSD 60

Db |||||

QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNV 120

Db |||||

QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNV 120

Db |||||

QY 121 GCDMPDGRLLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180

Db |||||

QY 121 GCDMPDGRLLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180

Db |||||

QY 181 LECECLELRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240

Db |||||

QY 181 LECECLELRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWOR 240

QY 241 DGEEOQTDELVELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300

Db 241 DGEQTDTELVELTRPAGDTGFKWAAVVPSEGEQYTCVHQHEGLPQPLILRWEQSPQ 300
Qy 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360
Db 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360
Qy 361 KV 362
Db 361 KV 362

RESULT 9
ADJ70081
ID ADJ70081 standard; protein; 442 AA.
AC ADJ70081;
XX
XX
DT 06-MAY-2004 (first entry)
DE Human heat mitochondrial protein as a therapeutic target SeqID1887.
XX
KW Mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW Mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
XX WO2003087768-A2.
XX
XX 23-OCT-2003.
XX
XX 04-APR-2003; 2003WO-US010870.
XX
XX 12-APR-2002; 2002US-0372843P.
XX 17-JUN-2002; 2002US-0389987P.
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW,
PI Warnock DE;
XX
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
XX Claim 1; SEQ ID NO 1887; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.

SQ Sequence 442 AA;
Query Match 67.4%; Score 244; DB 7; Length 442;
Best Local Similarity 99.7%; Pred. No. 5.7e-214;
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRGCGEPRIYAVEYVDDTQFLRFDSD 60
Db 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRGCGEPRIYAVEYVDDTQFLRFDSD 60
Qy 61 AAIPRMEPREPWEQEGPOYWEWTTGYAKANAQTDVRLNLLRRYVNSQSGSHTLQGMN 120
Db 61 AAIPRMEPREPWEQEGPOYWEWTTGYAKANAQTDVRLNLLRRYVNSQSGSHTLQGMN 120
Qy 121 GCDMPDGRLLRGYHQHAYDKDYISLNEDLRSWTAADTVAQITQRFYEAEEVPEPT 180
Db 121 GCDMPDGRLLRGYHQHAYDKDYISLNEDLRSWTAADTVAQITQRFYEAEEVPEPT 180
Qy 181 LECECELELLRRYLENGLETQRADPPKAVHHPISDHEATLRCWALGFYPAITLTMOR 240
Db 181 LECECELELLRRYLENGLETQRADPPKAVHHPISDHEATLRCWALGFYPAITLTMOR 240
Qy 241 DGEQTDTELVELTRPAGDTGFKWAAVVPSEGEQYTCVHQHEGLPQPLILRWEQSPQ 300
Db 241 DGEQTDTELVELTRPAGDTGFKWAAVVPSEGEQYTCVHQHEGLPQPLILRWEQSPQ 300
Qy 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAA 345
Db 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAA 345

RESULT 10
AAB43986
ID AAB43986 standard; protein; 271 AA.
XX
XX AAB43986;
XX
DT 08-FEB-2001 (first entry)
DE Human cancer associated protein sequence SEQ ID NO:1431.
XX
XX Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
KW antidiabetic; antiaesthetic; antirheumatic; antiallergic; antiviral;
KW antiinflammatory; antihypertoid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
XX Homo sapiens.
XX
XX WO200055350-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005882.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587533/55.
XX DR N-PSDB; AAC78195.
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer.
XX
XX Claim 11; Page 2115-2116; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
 CC AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnarary; immunomodulator;
 CC antidiabetic; antiaschmatic; antirheumatic; antibacterial;
 CC antiinflammatory; antihypertensive; antiallergic; thrombolytic; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancer, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 271 AA;

Query Match 54.1%; Score 196; DB 3; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.6e-170;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRPSD 60
 DB 7 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRPSD 66
 QY 61 AAIPRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 120
 DB 67 AAIPRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 126
 QY 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFRY 180
 DB 127 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFRY 186
 QY 181 LEGECLELLRRYLENG 196
 DB 187 LEGECLELLRRYLENG 202

RESULT 11
 ABG26726
 ID ABG26726 standard; protein; 677 AA.
 XX
 AC ABG26726;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #26717.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.
 DR N-PSDB; AAS90913.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 57085; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 677 AA;

Query Match 54.1%; Score 196; DB 4; Length 677;
 Best Local Similarity 100.0%; Pred. No. 5.5e-170;
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRPSD 60
 DB 310 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRPSD 369
 QY 61 AAIPRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 120
 DB 370 AAIPRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 429
 QY 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFRY 180
 DB 430 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFRY 489
 QY 181 LEGECLELLRRYLENG 196
 DB 490 LEGECLELLRRYLENG 505

RESULT 12
 AAG64618
 ID AAG64618 standard; protein; 274 AA.
 XX
 AC AAG64618;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 XX Human cancer cell specific HLA-F antigen SEQ ID 5.
 DE
 XX HLA-F antigen; cancer cell specific; human.
 KW
 XX Homo sapiens.
 OS
 XX JP2001095584-A.
 PN
 XX 10-APR-2001.
 PD

XX PF 30-SEP-1999; 99JP-00279566.
 XX PR 30-SEP-1999; 99JP-00279566.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA K.
 XX WPI; 2001-360493/38.
 DR N-PSDB; AAH45556.
 XX PT Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX PS Claim 2; Page 10-11; 12pp; Japanese.
 XX This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention

XX SQ Sequence 274 AA;
 Query Match 48.3%; Score 175; DB 4; Length 274;
 Best Local Similarity 100.0%; Pred. No. 3.9e-151;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 81
 DB 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60

QY 82 EWTGTGAKANAQTDRLVALNLLRRYNOSEAGSHTLQMGNCMDGPGRLLRGYHAYDG 141
 DB 61 EWTGTGAKANAQTDRLVALNLLRRYNOSEAGSHTLQMGNCMDGPGRLLRGYHAYDG 120

QY 142 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 196
 DB 121 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 175

RESULT 13
 ADF55588
 ID ADF55588 standard; protein; 274 AA.
 XX ADF55588;
 AC ADF55588;
 XX 12-FEB-2004 (first entry)
 XX Fragment #1 of human cancer-cell specific HLA-F antigen.
 XX Cancer; human leukocyte antigen-F; HLA-F;
 KW Cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
 KW major histocompatibility complex; MHC; cancer cell; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP2003012544-A.
 XX 15-JAN-2003.
 XX 27-MAR-2002; 2002JP-00088991.
 XX 27-MAR-2001; 2001JP-00090121.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA Y.
 XX WPI; 2003-486263/46.
 DR N-PSDB; ADF55585.

XX Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
 XX Claim 7; SEQ ID NO 5; 19pp; Japanese.
 XX The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HLA-F antigen.

XX SQ Sequence 274 AA;
 Query Match 48.3%; Score 175; DB 7; Length 274;
 Best Local Similarity 100.0%; Pred. No. 3.9e-151;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 81
 DB 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60

QY 82 EWTGTGAKANAQTDRLVALNLLRRYNOSEAGSHTLQMGNCMDGPGRLLRGYHAYDG 141
 DB 61 EWTGTGAKANAQTDRLVALNLLRRYNOSEAGSHTLQMGNCMDGPGRLLRGYHAYDG 120

QY 142 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 196
 DB 121 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 175

RESULT 14
 AAG64619
 ID AAG64619 standard; protein; 215 AA.
 XX AAG64619;
 AC AAG64619;
 XX 12-SEP-2001 (first entry)
 XX Human cancer cell specific HLA-F antigen SEQ ID 6.
 XX HLA-F antigen; cancer cell specific; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX JP2001095584-A.
 XX 10-APR-2001.
 XX 30-SEP-1999; 99JP-00279566.
 XX 30-SEP-1999; 99JP-00279566.
 XX (EGAW/) EGAWA K.
 PA (MEDI-) MEDINET KK.
 PA (KIMU/) KIMURA K.
 XX WPI; 2001-360493/38.
 DR N-PSDB; AAH45557.
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
 XX Claim 1; Page 11-12; 12pp; Japanese.
 XX This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the

CC preparation of the cancer cell specific HLA-F antigen. The antigen may be
CC used in a method to diagnose cancer, in which the protein is used to
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present
CC sequence represents the cancer cell-specific HLA-F antigen of the
CC invention

XX SQ Sequence 215 AA;
Query Match 42.3%; Score 153; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-131; Indels 0; Gaps 0;
Matches 153; Conservative 0; Mismatches 0;
QY 44 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEGPGYWEWTTGYAKANAQTDRLVALRNLL 103
Db 1 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEGPGYWEWTTGYAKANAQTDRLVALRNLL 60
QY 104 RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHAYDGGKDYISLNEDLRSWTAADTVAQI 163
Db 61 RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHAYDGGKDYISLNEDLRSWTAADTVAQI 120
QY 164 TORFYEAEEYAEFRTYLEGECELELLRRYLENG 196
Db 121 TORFYEAEEYAEFRTYLEGECELELLRRYLENG 153

RESULT 15
ADP55589
ID ADP55589 standard; protein; 215 AA.
XX AC ADP55589;
XX DT 12-FEB-2004 (first entry)
XX DE Fragment #2 of human cancer-cell specific HLA-F antigen.
XX KW Cancer; human leukocyte antigen-F; HLA-F;
XX KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
XX KW major histocompatibility complex; MHC; cancer cell; human.
XX OS Homo sapiens.
XX PN JP2003012544-A.
XX PD 15-JAN-2003.
XX PF 27-MAR-2002; 2002JP-00088991.
XX PR 27-MAR-2001; 2001JP-00090121.
XX PA (EGAW/) EGAWA K.
XX PA (MEDI-) MEDINET KK.
XX PA (KIMU/) KIMURA Y.
XX DR WPI; 2003-486263/46.
XX DR N-PSDB; ADP55586.
XX PT Agent for preventing and treating cancer, comprising human leukocyte
XX PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.
XX PS Claim 7; SEQ ID NO 6; 19pp; Japanese.
XX CC The present invention relates to an agent for preventing or treating
XX CC cancer. The agent comprises a portion or a complete sequence of a human
XX CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of
XX CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or
XX CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte
XX CC (CTL) inducer which induces CTL which is non-specific to an organ, is
XX CC unrestricted to the major histocompatibility complex (MHC) and specific
XX CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention
XX CC is useful for treating or preventing cancer. A cell capable of presenting
XX CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and
XX CC for diagnosing cancer. The present sequence represents part of the human
XX CC cancer-cell specific HLA-F antigen.

XX SQ Sequence 215 AA;
Query Match 42.3%; Score 153; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.9e-131; Indels 0; Gaps 0;
Matches 153; Conservative 0; Mismatches 0;
QY 44 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEGPGYWEWTTGYAKANAQTDRLVALRNLL 103
Db 1 IAVEYVDDTQFLRFDSDAAI PRMEPREPWVEGPGYWEWTTGYAKANAQTDRLVALRNLL 60
QY 104 RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHAYDGGKDYISLNEDLRSWTAADTVAQI 163
Db 61 RRYNQSEAGSHTLQGMNGCDMGPDGRLRLRGYHAYDGGKDYISLNEDLRSWTAADTVAQI 120
QY 164 TORFYEAEEYAEFRTYLEGECELELLRRYLENG 196
Db 121 TORFYEAEEYAEFRTYLEGECELELLRRYLENG 153

Search completed: July 13, 2005, 09:14:41
Job time : 168 secs